

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: FENG, YIQING
BAUM, CHARLES M
CAPARON, MAIRE H
ZURFLUH, LINDA L
KLEIN, BARBARA K
MCWHERTER, CHARLES A
STATEN, NICHOLAS R
SUMMERS, NEENA L
BAUER, S C
LEE, STEPHEN C
- (ii) TITLE OF INVENTION: MULTI-FUNCTIONAL HEMATOPOIETIC
FUSION PROTEINS BETWEEN SEQUENCE REARRANGED
G-CSF RECEPTOR AGONISTS AND OTHER
HEMATOPOIETIC FACTORS
- (iii) NUMBER OF SEQUENCES: 313
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: CAROL M. NIELSEN, GARDERE WYNNE SEWELL, LLP
 - (B) STREET: 1000 LOUISIANA, SUITE 3400
 - (C) CITY: HOUSTON
 - (D) STATE: TEXAS
 - (E) COUNTRY: USA
 - (F) ZIP: 77002-5007
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/510,238
 - (B) FILING DATE: 22-FEB-2002
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/835,162
 - (B) FILING DATE: 04-APR-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO PCT/US 96/15774
 - (B) FILING DATE: 06-OCT-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/004,834
 - (B) FILING DATE: 05-OCT-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: NIELSEN, CAROL M
 - (B) REGISTRATION NUMBER: 37,676

(C) REFERENCE/DOCKET NUMBER: 2910/3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 713-276-5383

(B) TELEFAX: 713-276-5383

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /note= "Xaa at position 1 is Thr, Ser, Arg, Tyr or Gly;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2

(D) OTHER INFORMATION: /note= "Xaa at position 2 is Pro or Leu;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 3

(D) OTHER INFORMATION: /note= "Xaa at position 3 is Leu, Arg, Tyr or Ser;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 13

(D) OTHER INFORMATION: /note= "Xaa at position 13 is Phe, Ser, His, Thr or Pro;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 16

(D) OTHER INFORMATION: /note= "Xaa at position 16 is Lys, Pro, Ser, thr or His;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 17

(D) OTHER INFORMATION: /note= "Xaa at position 17 is Cys, Ser, Gly, Ala, Ile, Tyr or Arg;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 18

(D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu, Thr, Pro, His, Ile or Cys;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 22
(D) OTHER INFORMATION: /note= "Xaa at position 22 is Arg,
Tyr, Ser, Thr or Ala;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 24
(D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile,
Pro, Tyr or Leu;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 27
(D) OTHER INFORMATION: /note= "Xaa at position 27 is Asp,
or Gly;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 30
(D) OTHER INFORMATION: /note= "Xaa at position 30 is Ala,
Ile, Leu or Gly;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 34
(D) OTHER INFORMATION: /note= "Xaa at position 34 is Lys
or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 36
(D) OTHER INFORMATION: /note= "Xaa at position 36 is Cys
or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 42
(D) OTHER INFORMATION: /note= "Xaa at position 42 is Cys
or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 43
(D) OTHER INFORMATION: /note= "Xaa at position 43 is His,
Thr, Gly, Val, Lys, Trp, Ala, Arg, Cys, or Leu;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 44
(D) OTHER INFORMATION: /note= "Xaa at position 44 is Pro,
Gly, Arg, Asp, Val, Ala, His, Trp, Gln, or Thr;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 46
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Glu,
Arg, Phe, Arg, Ile or Ala;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site

(B) LOCATION: 47
(D) OTHER INFORMATION: /note= "Xaa at position 47 is Leu
or Thr;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 49
(D) OTHER INFORMATION: /note= "Xaa at position 49 is Leu,
Phe, Arg or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 50
(D) OTHER INFORMATION: /note= "Xaa at position 50 is Leu,
Ile, His, Pro or Tyr;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 54
(D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu
or His;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 64
(D) OTHER INFORMATION: /note= "Xaa at position 64 is Cys
or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 67
(D) OTHER INFORMATION: /note= "Xaa at position 67 is Gln,
Lys, Leu or Cys;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 70
(D) OTHER INFORMATION: /note= "Xaa at position 70 is Gln,
Pro, Leu, Arg or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 74
(D) OTHER INFORMATION: /note= "Xaa at position 74 is Cys
or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 104
(D) OTHER INFORMATION: /note= "Xaa at position 104 is Asp,
Gly or Val;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 108
(D) OTHER INFORMATION: /note= "Xaa at position 108 is Leu,
Ala, Val, Arg, Trp, Gln or Gly;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 115

(D) OTHER INFORMATION: /note= "Xaa at position 115 is Thr, His, Leu or Ala;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 120

(D) OTHER INFORMATION: /note= "Xaa at position 120 is Gln, Gly, Arg, Lys or His"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 123

(D) OTHER INFORMATION: /note= "Xaa at position 123 is Glu, Arg, Phe or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 144

(D) OTHER INFORMATION: /note= "Xaa at position 144 is Phe, His, Arg, Pro, Leu, Gln or Glu;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 146

(D) OTHER INFORMATION: /note= "Xaa at position 146 is Arg or Gln;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 147

(D) OTHER INFORMATION: /note= "Xaa at position 147 is Arg or Gln;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 156

(D) OTHER INFORMATION: /note= "Xaa at position 156 is His, Gly or Ser;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 159

(D) OTHER INFORMATION: /note= "Xaa at position 159 is Ser, Arg, Thr, Tyr, Val or Gly;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 162

(D) OTHER INFORMATION: /note= "Xaa at position 162 is Glu, Leu, Gly or Trp;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 163

(D) OTHER INFORMATION: /note= "Xaa at position 163 is Val, Gly, Arg or Ala;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 169

(D) OTHER INFORMATION: /note= "Xaa at position 169 is Arg,

Ser, Leu, Arg or Cys;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 170

(D) OTHER INFORMATION: /note= "Xaa at position 170 is His, Arg or Ser;"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa	Xaa	Xaa	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Xaa	Leu	Leu	Xaa	
1				5				10					15			
Xaa	Xaa	Glu	Gln	Val	Xaa	Lys	Xaa	Gln	Gly	Xaa	Gly	Ala	Xaa	Leu	Gln	
		20				25						30				
Glu	Xaa	Leu	Xaa	Ala	Thr	Tyr	Lys	Leu	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Val	
		35				40						45				
Xaa	Xaa	Gly	His	Ser	Xaa	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Xaa	
		50				55				60						
Pro	Ser	Xaa	Ala	Leu	Xaa	Leu	Ala	Gly	Xaa	Leu	Ser	Gln	Leu	His	Ser	
65				70				75						80		
Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	
			85					90						95		
Pro	Glu	Leu	Gly	Pro	Thr	Leu	Xaa	Thr	Leu	Gln	Xaa	Asp	Val	Ala	Asp	
		100						105					110			
Phe	Ala	Xaa	Thr	Ile	Trp	Gln	Gln	Met	Glu	Xaa	Xaa	Gly	Met	Ala	Pro	
		115				120						125				
Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Xaa	
		130				135					140					
Gln	Xaa	Xaa	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	Xaa	Leu	Gln	Xaa	Phe	
145				150					155						160	
Leu	Xaa	Xaa	Ser	Tyr	Arg	Val	Leu	Xaa	Xaa	Leu	Ala	Gln	Pro			
			165					170								

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 17

(D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 18
 (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn,
His, Leu, Ile, Phe, Arg, or Gln;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 19
 (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met,
Phe, Ile, Arg, Gly, Ala, or Cys;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 20
 (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile,
Cys, Gln, Glu, Arg, Pro, or Ala;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 21
 (D) OTHER INFORMATION: /note= "Xaa at position 21 is Asp,
Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser or Val;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 22
 (D) OTHER INFORMATION: /note= "Xaa at position 22 is Glu,
Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val or Gly;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 23
 (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile,
Val, Ala, Gly, Trp, Lys, Phe, Leu, Ser, or Arg;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 24
 (D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile,
Gly, Val, Arg, Ser, Phe, Leu;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 25
 (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr,
His, Gly, Gln, Arg, Pro, or Ala;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 26
 (D) OTHER INFORMATION: /note= "Xaa at position 26 is His,
Thr, Phe, Gly, Arg, Ala, Trp;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 27
 (D) OTHER INFORMATION: /note= "Xaa at position 27 is Leu,
Gly, Arg, Thr, Ser, or Ala;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 28
(D) OTHER INFORMATION: /note= "Xaa at position 28 is Lys,
Arg, Leu, Gln, Gly, Pro, Val or Trp;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 29
(D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln,
Asn, Leu, Pro, Arg, or Val;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 30
(D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro,
His, Thr, Gly, Asp, Gln, Ser, Leu, or L..."

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 31
(D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro,
Asp, Gly, Ala, Arg, Leu, or Gln;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 32
(D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu,
Val, Arg, Gln, Asn, Gly, Ala, or Glu;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 33
(D) OTHER INFORMATION: /note= "Xaa at position 33 is Pro,
Leu, Gln, Ala, Thr, or Glu;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 34
(D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu,
Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile or Met;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 35
(D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu,
Ala, Gly, Asn, Pro, Gln, or Val;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 36
(D) OTHER INFORMATION: /note= "Xaa at position 36 is Asp,
Leu, or Val;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 37
(D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe,
Ser, Pro, Trp, or Ile;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site

(B) LOCATION: 38
(D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn,
or Ala;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 40
(D) OTHER INFORMATION: /note= "Xaa at position 40 is Leu,
Trp, or Arg;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 41
(D) OTHER INFORMATION: /note= "Xaa at position 41 is Asn,
Cys, Arg, Leu, His, Met, or pro;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 42
(D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,
Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr, Ile, Met
or Ala;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 43
(D) OTHER INFORMATION: /note= "Xaa at position 43 is Glu,
Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly, or Ser;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 44
(D) OTHER INFORMATION: /note= "Xaa at position 44 is Asp,
Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala or Pro;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 45
(D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,
Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg, Ser, Ala,
Ile, Glu or His;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 46
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp,
Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr, Ile, Val
or Gly;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 47
(D) OTHER INFORMATION: /note= "Xaa at position 47 is Ile,
Gly, Val, Ser, Arg, Pro, or His;"

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 48
(D) OTHER INFORMATION: /note= "Xaa at position 48 is Leu,
Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val or
Asn;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 49
 (D) OTHER INFORMATION: /note= "Xaa at position 49 is Met,
Arg, Ala, Gly, Pro, Asn, His, or Asp;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 50
 (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu,
Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met
or Gln;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 51
 (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn,
Arg, Met, Pro, Ser, Thr, or his;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 52
 (D) OTHER INFORMATION: /note= "Xaa at position 52 is Asn,
His, Arg, Leu, Gly, Ser, or Thr;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 53
 (D) OTHER INFORMATION: /note= "Xaa at position 53 is Leu,
Thr, Ala, Gly, Glu, Pro, Lys, Ser, or M..."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 54
 (D) OTHER INFORMATION: /note= "Xaa at position 54 is Arg,
Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala or Leu;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 55
 (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg,
Thr, Val, Ser, Leu, or Gly;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 56
 (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro,
Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val
or Lys;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 57
 (D) OTHER INFORMATION: /note= "Xaa at position 57 is Asn
or Gly;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 58
 (D) OTHER INFORMATION: /note= "Xaa at position 58 is Leu,

Ser, Asp, Arg, Gln, Val, or Cys;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 59

(D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu, Tyr, His, Leu, Pro, or Arg;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 60

(D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 61

(D) OTHER INFORMATION: /note= "Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 62

(D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or Ile;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 63

(D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or Val;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 64

(D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 65

(D) OTHER INFORMATION: /note= "Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 66

(D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 67

(D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His;"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 68

(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 69
 (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln,
Ala, Pro, Thr, Glu, Arg, Trp, Gly, or L..."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 70
 (D) OTHER INFORMATION: /note= "Xaa at position 70 is Asn,
Leu, Val, Trp, pro, or Ala;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 71
 (D) OTHER INFORMATION: /note= "Xaa at position 71 is Ala,
Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 72
 (D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser,
Glu, Met, Ala, His, Asn, Arg, or Asp;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 73
 (D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala,
Glu, Asp, Leu, Ser, Gly, Thr, or Arg;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 74
 (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ile,
Met, Thr, Pro, Arg, Gly, Ala;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 75
 (D) OTHER INFORMATION: /note= "Xaa at position 75 is Glu,
Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 76
 (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser,
Val, Ala, Asn, Trp, Glu, Pro, Gly, or A..."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 77
 (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile,
Ser, Arg, Thr, or Leu;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 78
 (D) OTHER INFORMATION: /note= "Xaa at position 78 is Leu,
Ala, Ser, Glu, Phe, Gly, or Arg;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 79
 (D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys,
Thr, Asn, Met, Arg, Ile, Gly, or Asp;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 80
 (D) OTHER INFORMATION: /note= "Xaa position at 80 is Asn,
Trp, Val, Gly, Thr, Leu, Glu, or Arg;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 81
 (D) OTHER INFORMATION: /note= "Xaa at position 81 is Leu,
Gln, Gly, Ala, Trp, Arg, Val, or Lys;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 82
 (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,
Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe,
Ile, Met or Val;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 83
 (D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro,
Ala, Thr, Trp, Arg, or Met;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 84
 (D) OTHER INFORMATION: /note= "Xaa at position 84 is Cys,
Glu, Gly, Arg, Met, or Val;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 85
 (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu,
Asn, Val, or Gln;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 86
 (D) OTHER INFORMATION: /note= "Xaa at position 86 is Pro,
Cys, Arg, Ala, or Lys;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 87
 (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu,
Ser, Trp, or Gly;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 88
 (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala,
Lys, Arg, Val, or Trp;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 89
 (D) OTHER INFORMATION: /note= "Xaa at position 89 is Thr,
Asp, Cys, Leu, Val, Glu, His, Asn, or S..."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 90
 (D) OTHER INFORMATION: /note= "Xaa at position 90 is Ala,
Pro, Ser, Thr, Gly, Asp, Ile, or ,Met;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 91
 (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala,
Pro, Ser, Thr, Phe, Leu, Asp, or His;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 92
 (D) OTHER INFORMATION: /note= "Xaa at position 92 is Pro,
Phe, Arg, Ser, Lys, His, Ala, Gly, Ile or Leu;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 93
 (D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr,
Asp, Ser, Asn, Pro, Ala, Leu, or Arg;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 94
 (D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg,
Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 95
 (D) OTHER INFORMATION: /note= "Xaa at position 95 is His,
Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe,
Ile, or Tyr;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 96
 (D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro,
Lys, Tyr, Gly, Ile, or Thr;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 97
 (D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile,
Val, Lys, Ala, or Asn;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 98
 (D) OTHER INFORMATION: /note= "Xaa at position 98 is His,
Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys,
Arg, Tyr, or Pro;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 99
 (D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 100
 (D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or ..."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 101
 (D) OTHER INFORMATION: /note= "Xaa at position is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 102
 (D) OTHER INFORMATION: /note= "Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 103
 (D) OTHER INFORMATION: /note= "Xaa at position 103 is Asp, or Ser;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 104
 (D) OTHER INFORMATION: /note= "Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala, Phe, or Gly;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 105
 (D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 106
 (D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or Pro;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 108
 (D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala or Pro;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 109
 (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or Gly;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 110
 (D) OTHER INFORMATION: /note= "Xaa at position 110 is Lys,
Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 111
 (D) OTHER INFORMATION: /note= "Xaa at position 111 is Leu,
Ile, Arg, Asp, or Met;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 112
 (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr,
Val, Gln, Tyr, Glu, His, Ser, or Phe;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 113
 (D) OTHER INFORMATION: /note= "Xaa at position 113 is Phe,
Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val or Asn;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 114
 (D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr,
Cys, His, Ser, Trp, Arg, or Leu;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 115
 (D) OTHER INFORMATION: /note= "Xaa at position 115 is Leu,
Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 116
 (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys,
Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala,
Tyr, Phe, Gln, or Ile;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 117
 (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr,
Ser, Asn, Ile, Trp, Lys, or Pro;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 118
 (D) OTHER INFORMATION: /note= "Xaa at position 118 is Leu,
Ser, Pro, Ala, Glu, Cys, Asp, or Tyr;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 119
 (D) OTHER INFORMATION: /note= "Xaa at position 119 is Glu,
Ser, Lys, Pro, leu, Thr, Tyr, or Arg;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 120
 (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 121
 (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 122
 (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys;"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 123
 (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu;"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys	
1				5					10					15		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25					30			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			35				40					45				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			50				55				60					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70					75						80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85					90					95		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105					110			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Gln	Thr	Thr	Leu	
			115				120					125				
Ser	Leu	Ala	Ile	Phe												
			130													

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 332 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 112

(D) OTHER INFORMATION: /note= "position 112 is deleted or Leu, Ala, Val, Ile, Pro, Phe, Trp, or M..."

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 113

(D) OTHER INFORMATION: /note= "position 113 is deleted or Pro, Phe, Ala, Leu, Ile, Trp, or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 114

(D) OTHER INFORMATION: /note= "position 114 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 115

(D) OTHER INFORMATION: /note= "position 115 is deleted or Gln, Gly, Ser, Thr, Tyr or Asn"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys	Leu	Leu	
1				5					10					15		
Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro	Glu	Val	
			20					25					30			
His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	
		35				40					45					
Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	
	50					55					60					
Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	
65				70					75						80	
Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	
				85				90					95			
Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Xaa	
		100					105						110			
Xaa	Xaa	Xaa	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	
		115					120					125				
Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	
	130					135					140					
Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr	Ala	
145					150					155					160	

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /note= "where x=(glyglyglyglyser)n
and where n is an interger"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Ala Ala
1

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /note= "where Xaa
=(glyglyglyglyglyser)n and where n is an integer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Xaa Ala Ala
1

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /note= "where xaa = (gly(n)ser)m
and where n is an integer and m is an int..."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

1

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

- ```
(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /note= "where Xaa=(alaglyser)n and
where n is an integer"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

1

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

1 5 10 15 20 25 30 35

Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser

Gly Gly Gly Ser

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ile Ser Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro  
1 5 10 15  
Ser Lys Glu Ser His Lys Ser Pro  
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ile Glu Gly Arg Ile Ser Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn  
1 5 10 15  
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
20 25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Gly Gly Ser  
1

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACGTCCATGG CNTCNCCNGC NCCNCCTGCT TGTGCACTCC GAGTC  
45

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGCACGAAT TCCCTGACGC AGAGGGTGA  
30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGACAAGCTT ACCTGACGCA GAGGGTGGAC CCT  
33

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATTCGGCAA  
10

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CATGTTGCCG  
10

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATTCGGCGG CAA  
13

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CATGTTGCCG CCG  
13

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:  
AATTCGGCGG CAACGGCGGC AA  
22

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:  
CATGTTGCCG CCGTTGCCGC CG  
22

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:  
CGATCCATGG AGGTTACCCC TTTGCCT  
27

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATCAAGCTT ATGGGCACTG GCTCAGTCT  
29

- (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGATACATGT TGCCTACACC TGTCCTG  
27

- (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATCAAGCTT AAGGGTGAAC CTCTGGGCA  
29

- (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGATCCATGG TCCTGCTGCC TGCTGTG  
27

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GATCAAGCTT AAGGTGTAGG CAAAGGGTG  
29

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGATCCATGG CTGTGGACTT TAGCTTGGA  
30

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCAAGCTT AAGGCAGCAG GACAGGTGT  
29

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGATCCATGG ACTTTAGCTT GGGAGAA  
27

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GATCAAGCTT ACACAGCAGG CAGCAGGAC  
29

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGATCCATGG GAGAATGGAA AACCCAG

27

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GATCAAGCTT ACAAGCTAAA GTCCACAGC  
29

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CGATCCATGG GACCCACTTG CCTCTCA  
27

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCAAGCTT ACAGTTGTCC CCGTGCTGC  
29

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGTCCATGG GAACCCAGCT TCCTCCA  
27

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATCAAGCTT AAAGGAGGCT CTGCAGGGC  
29

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGATCCATGG GCAGGACCAC AGCTCAC  
27

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCAAGCTT ACTGTGGAGG AAGCTGGGTT  
30

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGATCCATGG CTCACAAGGA TCCCAATGCC  
30

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCAAGCTT ATGTGGTCCT GCGCTGTGG  
29

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CGATCCATGG ATCCCAATGC CATCTTCCTG  
30

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATCAAGCTT ACTTGTGAGC TGTGGTCCT  
29

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGATCCATGG CCATCTTCCT GAGCTTCCAA  
30

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATCAAGCTT AATTGGGATC CTTGTGAGCT GT  
32

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AATTCCGTCG TAAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT  
60

ACGTAGAGGG CGGTGGAGGC TCC  
83

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCGGGGAGCC TCCACCGCCC TCTACGTACT GTTAGCCTG CGCGTTCTCC AAGGTTTCA  
60

GATAGAAGGT CAGTTTACGA CGG  
83

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTAAGTCTC TATAATGAT  
59

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGATCATTAT AGAGCAGTTA GAGCCACCAC CCTGTTGTTC CTGCGCTTGC TCAAGG  
56

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTGGCGGTGG CAGCGGCGGC  
60

GGTTCTAACT GCTCTATAAT  
80

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGATCATTAT AGAGCAGTTA GAACCGCCGC CGCTGCCACC GCCAGAGCCA CCACCCTGTT  
60

G TTCCTGCGC TTGCTCAAGG  
80

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCGACCAT GGCTCTGGAC CCGAACAACC  
30

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTCGATTACG TACAAAGGTG CAGGTGGT  
28

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GATCGACCAT GGCTAATGCA TCAGGTATTG AG  
32

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTCGATTACG TATTCTAAGT TCTTGACA  
28

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GATCGACCAT GGCTGCACCC TCTCGACATC CA  
32

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTCGATTACG TAGGCCGTGG CAGAGGGC  
28

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GATCGACCAT GGCTGCAGGT GACTGGCAAG AA  
32

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CTCGATTACG TACTTGATGA TGATTGGA  
28

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GCTCTGAGAG CCGCCAGAGC CGCCAGAGGG CTGCGCAAGG TGGCGTAGAA CGCG  
54

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAG  
54

- (2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGGCTGCGCA AGGTGGCG  
18

- (2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACACCATTGG GCCCTGCCAG C  
21

- (2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GATCGACCAT GGCTTACAAG CTGTGCCACC CC  
32

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CGATCGAAGC TTATTAGGTG GCACACAGCT TCTCCT  
36

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GATCGACCAT GGCTCCCGAG TTGGGTCCCA CC  
32

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CGATCGAAGC TTATTAGGAT ATCCCTTCCA GGGCCT  
36

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GATCGACCAT GGCTATGGCC CCTGCCCTGC AG  
32

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CGATCGAAGC TTATTATCCC AGTTCTTCCA TCTGCT  
36

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GATCGACCAT GGCTACCCAG GGTGCCATGC CG  
32

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CGATCGAAGC TTATTAGGGC TGCAGGGCAG GGGCCA  
36

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CGATCGAAGC TTATTAGGGC TGCAGGGCAG GGGCCA  
36

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CGATCGAAGC TTATTAGGCG AAGGCCGGCA TGGCAC  
36

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTAGAGGGCG GTGGAGGCTC C  
21

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCGGGGAGCC TCCACCGCCC TCTAC  
25

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTCTACGCCA CCTTGCGCAG CCCGGCGGCG GCTCTGACAT GTCTACACCA TTG  
53

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CAATGGTGTA GACATGTCAG AGCCGCCGCC GGGCTGCGCA AGGTGGCGTA GAA  
53

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 439 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGT  
439

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 465 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCCCAGCTC CACCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGA TCTCCCAT  
60

GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTTACC CTTTGCCTAC ACCTGTCCTG  
120

CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA  
180

CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA  
240

CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC  
300

CTTGGGGCCC TGCAGAGCCT CTTTGAAC CAGCTTCCTC CACAGGGCAG GACCACAGCT  
360

CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT  
420

TTCCTGATGC TTGTAGGAGG GTCCACCCTC TGCCTCAGGG AATTC  
465

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 927 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCCCCAGCTC CACCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGA TCTCCCAT  
60

GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTTACC CTTTGCCTAC ACCTGTCCTG  
120

CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA  
180

CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA  
240

CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC  
300

CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT  
360

CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT  
420

TTCCTGATGC TTGTAGGAGG GTCCACCCTC TGCGTCAGGG AATTCGGCGG CAACATGGCG  
480

TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGACTCCCAT  
540

GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACCC CTTTGCCTAC ACCTGTCCTG  
600

CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA  
660

CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA  
720

CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC  
780

CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGGGCAGGA CCACAGCTCA CAAGGATCCC  
840

AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT CCTGATGCTT  
900

GTAGGAGGGT CCACCCTCTG CGTCAGG  
927

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 936 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCCCCAGCTC CACCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGACTCCCAT  
60

GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACCC CTTTGCCTAC ACCTGTCCTG  
120

CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA  
180

CAGGACATTC TGGGAGCAGT GACCCCTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA  
240

CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC  
300

CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT  
360

CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT  
420

TTCCTGATGC TTGTAGGAGG GTCCACCCTC TGCCTCAGGG AATTCGGCAA CATGGCGTCT  
480

CCCCTCCGC CTGCTTGTA CCTCCGAGTC CTCAGTAAAC TGCTTCGTGA CTCCCATGTC  
540

CTTCACAGCA GACTGAGCCA GTGCCAGAG GTTACCCTT TGCCTACACC TGTCTGCTG  
600

CCTGCTGTGG ACTTTAGCTT GGGAGAATGG AAAACCCAGA TGGAGGAGAC CAAGGCACAG  
660

GACATTCTGG GAGCAGTGAC CCTTCTGCTG GAGGGAGTGA TGGCAGCACG GGGACAACTG  
720

GGACCCACTT GCCTCTCATC CCTCCTGGGG CAGCTTTCTG GACAGGTCCG TCTCCTCCTT  
780

GGGGCCCTGC AGAGCCTCCT TGAACCCAG CTCCTCCAC AGGGCAGGAC CACAGCTCAC  
840

AAGGATCCCA ATGCCATCTT CCTGAGCTTC CAACACCTGC TCCGAGGAAA GGTGCGTTTC  
900

CTGATGCTTG TAGGAGGGTC CACCCTCTGC GTCAGG  
936

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TCCCCAGCTC CACCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGA TCCCAT  
60

GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACC CTTGCTTAC ACCTGTCCTG  
120

CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA  
180

CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA  
240

CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC  
300

CTTGGGGCCC TGCAGAGCCT CCTTGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT  
360

CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT  
420

TTCCTGATGC TTGTAGGAGG GTCCACCCTC TCGTCAGGG AATTCGGCGG CAACATGGCG  
480

TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGACTCCCAT  
540

GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACCC CTTTGCCTAC ACCTGTCCTG  
600

CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA  
660

CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA  
720

CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC  
780

CTTGGGGCCC TGCAGAGCCT CCTTGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT  
840

CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT  
900

TTCCTGATGC TTGTAGGAGG GTCCACCCTC TCGTCAGG  
939

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 948 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TCCCCAGCGC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGACTCCCAT  
60

GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACC CTTGCCTAC ACCTGTCCTG  
120

CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA  
180

CAGGACATTC TGGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA  
240

CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC  
300

CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT  
360

CACAAGGATC CCAATGCCAT CTCCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT  
420

TTCCTGATGC TTGTAGGAGG GTCCACCTC TCGTCAGGG AATTCGGCGG CAACGGCGGC  
480

AACATGGCGT CCCCAGCGCC GCCTGCTTGT GACCTCCGAG TCCTCAGTAA ACTGCTTCGT  
540

GACTCCCATG TCCTTCACAG CAGACTGAGC CAGTGCCCAG AGGTTCACCC TTTGCCTACA  
600

CCTGTCCTGC TGCCTGCTGT GGACTTTAGC TTGGGAGAAT GGAAAACCCA GATGGAGGAG  
660

ACCAAGGCAC AGGACATTCT GGGAGCAGTG ACCCTTCTGC TGGAGGGAGT GATGGCAGCA  
720

CGGGGACAAC TGGGACCCAC TTGCCTCTCA TCCCTCCTGG GGCAGCTTTC TGGACAGGTC  
780

CGTCTCCTCC TTGGGGCCCT GCAGAGCCTC CTTGGAACCC AGCTTCCTCC ACAGGGCAGG  
840

ACCACAGCTC ACAAGGATCC CAATGCCATC TTCCTGAGCT TCCAACACCT GCTCCGAGGA  
900

AAGGTGCGTT TCCTGATGCT TGTAGGAGGG TCCACCCTCT GCGTCAGG  
948

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CATGGCTAAC TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTGC  
60

ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC TCTATCCTGA TGGACCGAAA  
120

CCTTCGACTT CCAAACCTGG AGAGCTTCGT AAGGGCTGTC AAGAACTTAG AAAATGCATC  
180

AGGTATTGAG GCAATTCTTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC  
240

CTCTCGACAT CCAATCATCA TCAAGGCAGG TGACTGGCAA GAATTCCGGG AAAAACTGAC  
300

GTTCTATCTG GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTAAGTGTCTC  
360

TATAATGATC GATGAAATTA TACATCACTT AAAGAGACCA CCTGCACCTT TGCTGGACCC  
420

GAACAACCTC AATGACGAAG ACGTCTCTAT CCTGATGGAC CGAAACCTTC GACTTCCAAA  
480

CCTGGAGAGC TTCGTAAGGG CTGTCAAGAA CTTAGAAAAT GCATCAGGTA TTGAGGCAAT  
540

TCTTCGTAAT CTCCAACCAT GTCTGCCCTC TGCCACGGCC GCACCCTCTC GACATCCAAT  
600

CATCATCAAG GCAGGTGACT GGCAAGAATT CCGGGAAAAA CTGACGTTCT ATCTGGTTAC  
660

CCTTGAGCAA GCGCAGGAAC AACAGTAC  
688

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 712 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CATGGCTAAC TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTGC  
60

ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC TCTATCCTGA TGGACCGAAA  
120

CCTTCGACTT CCAAACCTGG AGAGCTTCGT AAGGGCTGTC AAGAACTTAG AAAATGCATC  
180

AGGTATTGAG GCAATTCTTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC  
240

CTCTCGACAT CCAATCATCA TCAAGGCAGG TGACTGGCAA GAATTCCGGG AAAAAGTGAC  
300

GTTCTATCTG GTTACCCTTG AGCAAGCGCA GGAACAACAG GGTGGTGGCT CTGGCGGTGG  
360

CAGCGGCGGC GGTCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG  
420

ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT  
480

GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA  
540

AAATGCATCA GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC  
600

GGCCGCACCC TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA  
660

AAAAAGTGACG TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT AC  
712

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATGGCTCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
60

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
120

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
180

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAAGTGACG  
240

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGG GTGGTGGCTC TAACTGCTCT  
300

ATAATGATCG ATGAAATTAT ACATCACTTA AAGAGACCAC CTGCACCTTT GTACGTAGAG  
360

GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT  
420

CCGTCTAAAG AATCTCATAA ATCTCCAAAC ATGGCTACCC AGGGTGCCAT GCCGGCCTTC  
480

GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCTTGGTTG CTAGCCATCT GCAGAGCTTC  
540

CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC  
600

TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG CGATGGCGCA  
660

GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG  
720

CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG  
780

CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG  
840

CAGGCCCTGG AAGGGATATC CCCCAGATTG GGTCCCACCT TGGACACACT GCAGCTGGAC  
900

GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT GGCCCCTGCC  
960

CTGCAGCCCT AATAA  
975

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 975 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATGGCTCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
60

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
120

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
180

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
240

TTCTATCTGG TTACCTTGA GCAAGCGCAG GAACAACAGG GTGGTGGCTC TAACTGCTCT  
300

ATAATGATCG ATGAAATTAT ACATCACTTA AAGAGACCAC CTGCACCTTT GTACGTAGAG  
360

GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT  
420

CCGTCTAAAG AATCTCATAA ATCTCCAAAC ATGGCTACCC AGGGTGCCAT GCCGGCCTTC  
480

GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCTTGTTG CTAGCCATCT GCAGAGCTTC  
540

CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC  
600

TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG CGATGGCGCA  
660

GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG  
720

CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG  
780

CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG  
840

CAGGCCCTGG AAGGGATATC CCCCAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC  
900

GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT GGCCCCTGCC  
960

CTGCAGCCCT AATAA  
975

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

ATGGCTGCAC CCTCTCGACA TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG  
60

GAAAACTGA CGTTCTATCT GGTTACCCTT GAGCAAGCGC AGGAACAACA GGGTGGTGGC  
120

TCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
180

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
240

CGACTTCCAA ACCTGGAGAG CTTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
300

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CTACGTAGAG  
360

GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT  
420

CCGTCTAAAG AATCTCATAA ATCTCCAAAC ATGGCTACCC AGGGTGCCAT GCCGGCCTTC  
480

GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCTTGTTG CTAGCCATCT GCAGAGCTTC  
540

CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC  
600

TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG CGATGGCGCA  
660

GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG  
720

CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG  
780

CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG  
840

CAGGCCCTGG AAGGGATATC CCCCAGATTG GGTCCCACCT TGGACACACT GCAGCTGGAC  
900

GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT GGCCCCTGCC  
960

CTGCAGCCCT AATAA  
975

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGGCTGCAG GTGACTGGCA AGAATTCCGG GAAAACTGA CGTTCTATCT GGTTACCCTT  
60

GAGCAAGCGC AGGAACAACA GGGTGGTGGC TCTAACTGCT CTATAATGAT CGATGAAATT  
120

ATACATCACT TAAAGAGACC ACCTGCACCT TTGCTGGACC CGAACAACCT CAATGACGAA  
180

GACGTCTCTA TCCTGATGGA CCGAAACCTT CGACTTCCAA ACCTGGAGAG CTTCGTAAGG  
240

GCTGTCAAGA ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA  
300

TGTCTGCCCT CTGCCACGGC CGCACCTCTT CGACATCCAA TCATCATCAA GTACGTAGAG  
360

GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT  
420

CCGTCTAAAG AATCTCATAA ATCTCCAAAC ATGGCTACCC AGGGTGCCAT GCCGGCCTTC  
480

GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC  
540

CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC  
600

TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG CGATGGCGCA  
660

GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG  
720

CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG  
780

CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG  
840

CAGGCCCTGG AAGGGATATC CCCCAGATTG GGTCCCACCT TGGACACACT GCAGCTGGAC  
900

GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT GGCCCCTGCC  
960

CTGCAGCCCT AATAA  
975

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 999 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATGGCTCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
60  
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
120  
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
180  
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
240  
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGG GTGGTGGCTC TGGCGGTGGC  
300  
AGCGGCGGCG GTTCTAACTG CTCTATAATG ATCGATGAAA TTATACATCA CTTAAAGAGA  
360  
CCACCTGCAC CTTTGTACGT AGAGGGCGGT GGAGGCTCCC CGGGTGAACC GTCTGGTCCA  
420  
ATCTCTACTA TCAACCCGTC TCCTCCGTCT AAAGAATCTC ATAAATCTCC AAACATGGCT  
480  
ACCCAGGGTG CCATGCCGGC CTTGCTCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTCTG  
540  
GTTGCTAGCC ATCTGCAGAG CTTCTGAGG GTGTCTGACC GCGTTCTACG CCACCTTGCG  
600  
CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG  
660  
AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG  
720  
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG  
780  
AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC  
840  
CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC  
900  
ACCTTGACCA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG  
960  
GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA  
999

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 999 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ATGGCTAATG CATCAGGTAT TGAGGCAATT CTTCGTAATC TCCAACCATG TCTGCCCTCT  
60  
GCCACGGCCG CACCCTCTCG ACATCCAATC ATCATCAAGG CAGGTGACTG GCAAGAATTC  
120  
CGGGAAAAAC TGACGTTCTA TCTGGTTACC CTTGAGCAAG CGCAGGAACA ACAGGGTGGT  
180  
GGCTCTGGCG GTGGCAGCGG CGGCGGTTCT AACTGCTCTA TAATGATCGA TGAAATTATA  
240  
CATCACTTAA AGAGACCACC TGCACCTTTG CTGGACCCGA ACAACCTCAA TGACGAAGAC  
300  
GTCTCTATCC TGATGGACCG AAACCTTCGA CTTCCAAACC TGGAGAGCTT CGTAAGGGCT  
360  
GTCAAGAACT TAGAATACGT AGAGGGCGGT GGAGGCTCCC CGGGTGAACC GTCTGGTCCA  
420  
ATCTCTACTA TCAACCCGTC TCCTCCGTCT AAAGAATCTC ATAAATCTCC AAACATGGCT  
480  
ACCCAGGGTG CCATGCCGGC CTTGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTCTG  
540  
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG  
600  
CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG  
660  
AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG  
720  
TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCCTG GGCTCCCCCTG  
780  
AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC  
840  
CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC  
900  
ACCTTGGA CA CTGTCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG  
960

GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA  
999

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGGCTGCAC CCTCTCGACA TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG  
60

GAAAAACTGA CGTTCTATCT GGTTACCCTT GAGCAAGCGC AGGAACAACA GGGTGGTGGC  
120

TCTGGCGGTG GCAGCGGCGG CGGTTCTAAC TGCTCTATAA TGATCGATGA AATTATACAT  
180

CACTTAAAGA GACCACCTGC ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC  
240

TCTATCCTGA TGGACCGAAA CCTTCGACTT CCAAACCTGG AGAGCTTCGT AAGGGCTGTC  
300

AAGAACTTAG AAAATGCATC AGGTATTGAG GCAATTCTTC GTAATCTCCA ACCATGTCTG  
360

CCCTCTGCCA CGGCCTACGT AGAGGGCGGT GGAGGCTCCC CGGGTGAACC GTCTGGTCCA  
420

ATCTCTACTA TCAACCCGTC TCCTCCGTCT AAAGAATCTC ATAAATCTCC AAACATGGCT  
480

ACCCAGGGTG CCATGCCGGC CTTGCTCTCT GCTTTCAGC GCCGGGCAGG AGGGGTCCTG  
540

GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG  
600

CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG  
660

AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG  
720

TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG  
780

AGTCCTTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC  
840

CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC  
900

ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG  
960

GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA  
999

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGGCTGCAG GTGACTGGCA AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTACCCCTT  
60

GAGCAAGCGC AGGAACAACA GGGTGGTGGC TCTGGCGGTG GCAGCGGCGG CGGTTCTAAC  
120

TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTGC ACCTTTGCTG  
180

GACCCGAACA ACCTCAATGA CGAAGACGTC TCTATCCTGA TGGACCGAAA CCTTCGACTT  
240

CCAAACCTGG AGAGCTTCGT AAGGGCTGTC AAGAACTTAG AAAATGCATC AGGTATTGAG  
300

GCAATTCTTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC CTCTCGACAT  
360

CCAATCATCA TCAAGTACGT AGAGGGCGGT GGAGGCTCCC CGGGTGAACC GTCTGGTCCA  
420

ATCTCTACTA TCAACCCGTC TCCTCCGTCT AAAGAATCTC ATAAATCTCC AAACATGGCT  
480

ACCCAGGGTG CCATGCCGGC CTTGCGCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTCTG  
540

GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG  
600

CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG  
660

AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG  
720

TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG  
780

AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC  
840

CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC  
900

ACCTTGACAC CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG  
960

GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA  
999

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT ACAAGCTGTG CCACCCCGAG  
420

GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC  
480

AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCTCTAC  
540

CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCGAGT TGGGTCCCAC CTTGGACACA  
600

CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA  
660

ATGGCCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG CCTTCGCCTC TGCTTTCCAG  
720

CGCCGGGCAG GAGGGGTCCT GGTGCTAGC CATCTGCAGA GCTTCCTGGA GGTGTCGTAC  
780

CGCGTTCTAC GCCACCTTGC GCAGCCCTCT GGCGGCTCTG GCGGCTCTCA GAGCTTCCTG  
840

CTCAAGTCTT TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG  
900

CTGTGTGCCA CCTAATAA  
918

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 963 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC  
480

GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG  
540

CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG  
600

GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC  
660

GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCCTG  
720

CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG  
780

GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC  
840

CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG  
900

CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAA  
960

TAA  
963

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC CCGAGTTGGG TCCCACCTTG  
420

GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA GATGGAAGAA  
480

CTGGGAATGG CCCCTGCCCT GCAGCCCACC CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT  
540

TTCCAGCGCC GGGCAGGAGG GGTCTGGTT GCTAGCCATC TGCAGAGCTT CCTGGAGGTG  
600

TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCTCTGGCG GCTCTGGCGG CTCTCAGAGC  
660

TTCCTGCTCA AGTCTTTAGA GCAAGTGAGA AAGATCCAGG GCGATGGCGC AGCGCTCCAG  
720

GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC  
780

TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA  
840

GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG  
900

GAAGGGATAT CCTAATAA  
918

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG  
480

GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCCT  
540

GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA  
600

GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA  
660

CGCCACCTTG CGCAGCCCTC TGGCGGCTCT GGCGGCTCTC AGAGCTTCCT GCTCAAGTCT  
720

TTAGAGCAAG TGAGAAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC  
780

ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG GACACTCTCT GGGCATCCCC  
840

TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA  
900

CTCCATAGCG GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCTAA  
960

TAA  
963

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA TGGCCCCTGC CCTGCAGCCC  
420

ACCCAGGGTG CCATGCCGGC CTTGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG  
480

GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG  
540

CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG  
600

AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG  
660

TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG  
720

AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC  
780

CTTTTCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCGA GTTGGGTCCC  
840

ACCTTGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG  
900

GAAGAACTGG GATAATAA  
918

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TTCATAAAT CTCCAAACAT GGCTATGGCC CCTGCCCTGC AGCCCACCCA GGGTGCCATG  
480

CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG  
540

CAGAGCTTCC TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CTCTGGCGGC  
600

TCTGGCGGCT CTCAGAGCTT CCTGCTCAAG TCTTTAGAGC AAGTGAGAAA GATCCAGGGC  
660

GATGGCGCAG CGCTCCAGGA GAAGCTGTGT GCCACCTACA AGCTGTGCCA CCCCAGGAG  
720

CTGGTGCTGC TCGGACACTC TCTGGGCATC CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC  
780

CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC CAACTCCATA GCGGCCTTTT CCTCTACCAG  
840

GGGCTCCTGC AGGCCCTGGA AGGGATATCC CCCGAGTTGG GTCCCACCTT GGACACACTG  
900

CAGCTGGACG TCGCCGACTT TGCCACCACC ATCTGGCAGC AGATGGAAGA ACTGGGATAA  
960

TAA  
963

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 918 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CCCAGGGTGC CATGCCGGCC  
420

TTGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC  
480

TTCTTGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCTCTGG CGGCTCTGGC  
540

GGCTCTCAGA GCTTCTGCT CAAGTCTTTA GAGCAAGTGA GAAAGATCCA GGGCGATGGC  
600

GCAGCGCTCC AGGAGAAGCT GTGTGCCACC TACAAGCTGT GCCACCCCGA GGAGCTGGTG  
660

CTGCTCGGAC ACTCTCTGGG CATCCCCTGG GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC  
720

CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA CCAGGGGCTC  
780

CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG  
840

GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCCT  
900

GCCCTGCAGC CCTAATAA  
918

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
 120  
 CTTGCACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
 300  
 TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
 360  
 TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
 420  
 TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC  
 480  
 CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTGC  
 540  
 TACCGCGTTC TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC  
 600  
 CTGCTCAAGT CTTTAGAGCA AGTGAGAAAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG  
 660  
 AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT  
 720  
 CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC  
 780  
 TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA  
 840  
 GGGATATCCC CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT  
 900  
 GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCTAA  
 960  
 TAA  
 963

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 918 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT CTGCTTTCCA GCGCCGGGCA  
420

GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA  
480

CGCCACCTTG CGCAGCCCTC TGGCGGCTCT GGCGGCTCTC AGAGCTTCCT GCTCAAGTCT  
540

TTAGAGCAAG TGAGAAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC  
600

ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG GAACTCTCT GGGCATCCCC  
660

TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA  
720

CTCCATAGCG GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCCCC  
780

GAGTTGGGTC CCACCTTGGA CAACTGCAG CTGGACGTCG CCGACTTTGC CACCACCATC  
840

TGGCAGCAGA TGGAAGAACT GGAATGGCC CCTGCCCTGC AGCCACCCA GGGTGCCATG  
900

CCGGCCTTCG CCTAATAA  
918

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTTCTGCT TTCCAGCGCC GGGCAGGAGG GGTCTTGTT  
480

GCTAGCCATC TGCAGAGCTT CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG  
540

CCCTCTGGCG GCTCTGGCGG CTCTCAGAGC TTCTGCTCA AGTCTTTAGA GCAAGTGAGA  
600

AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC  
660

CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC  
720

TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT  
780

TTCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC  
840

TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA  
900

GAACTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTAA  
960

TAA  
963

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 927 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA
60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC
120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA
180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC
240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC
360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT ACAAGCTGTG CCACCCCGAG
420
GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC
480
AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCTCTAC
540
CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCGAGT TGGGTCCCAC CTTGGACACA
600
CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA
660
ATGGCCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG CCTTCGCCTC TGCTTTCCAG
720
CGCCGGGCAG GAGGGGTCCT GGTGCTAGC CATCTGCAGA GCTTCCTGGA GGTGTCGTAC
780
CGCGTTCTAC GCCACCTTGC GCAGCCCACA CCATTGGGCC CTGCCAGCTC CCTGCCCCAG
840
AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC
900
CAGGAGAAGC TGTGTGCCAC CTAATAA
```

927

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC  
480

GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG  
540

CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GTCCTGCAG  
600

GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC  
660

GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG  
720

CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG  
780

GTCTTGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC  
840

CTTGCGCAGC CCACACCAT GGGCCCTGCC AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG

900

TCTTTAGAGC AAGTGAGAAA GATCCAGGGC GATGGCGCAG CGCTCCAGGA GAAGCTGTGT  
960

GCCACCTAAT AA  
972

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC CCGAGTTGGG TCCCACCTTG  
420

GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA GATGGAAGAA  
480

CTGGGAATGG CCCCTGCCCT GCAGCCCACC CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT  
540

TTCCAGCGCC GGGCAGGAGG GGTCTGGTT GCTAGCCATC TGCAGAGCTT CCTGGAGGTG  
600

TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCACACCAT TGGGCCCTGC CAGCTCCCTG  
660

CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG CGATGGCGCA  
720

GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG

780

CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG  
840

CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG  
900

CAGGCCCTGG AAGGGATATC CTAATAA  
927

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG  
480

GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCCT  
540

GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA  
600

GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA  
660

CGCCACCTTG CGCAGCCCAC ACCATTGGGC CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG

720

CTCAAGTCTT TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG  
780

CTGTGTGCCA CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG AACTCTCTG  
840

GGCATCCCCCT GGGCTCCCCT GAGCTCCTGC CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC  
900

TTGAGCCAAC TCCATAGCGG CCTTTTCCTC TACCAGGGGC TCCTGCAGGC CCTGGAAGGG  
960

ATATCCTAAT AA  
972

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA TGGCCCCTGC CCTGCAGCCC  
420

ACCCAGGGTG CCATGCCGGC CTTGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTCTG  
480

GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG  
540

CAGCCCACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA

600

GAGCAAGTGA GAAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC  
660

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG  
720

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC  
780

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGAAGGGAT ATCCCCGAG  
840

TTGGGTCCCA CCTTGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG  
900

CAGCAGATGG AAGAACTGGG ATAATAA  
927

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA (synthetic)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTATGGCC CCTGCCCTGC AGCCCACCCA GGGTGCCATG  
480

CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG

540

CAGAGCTTCC TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CACACCATTG  
600

GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGAAAAG  
660

ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC  
720

CCCGAGGAGC TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC  
780

TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG CGGCCTTTTC  
840

CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC CCGAGTTGGG TCCCACCTTG  
900

GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA GATGGAAGAA  
960

CTGGGATAAT AA  
972

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CCCAGGGTGC CATGCCGGCC

420

TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC  
480

TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCACACC ATTGGGGCCCT  
540

GCCAGCTCCC TGCCCCAGAG CTTCTGCTC AAGTCTTTAG AGCAAGTGAG AAAGATCCAG  
600

GGCGATGGCG CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG CCACCCCGAG  
660

GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC  
720

AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCTCTAC  
780

CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCGAGT TGGGTCCCAC CTTGGACACA  
840

CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA  
900

ATGGCCCCCTG CCCTGCAGCC CTAATAA  
927

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC

360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC  
480

CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCTG  
540

TACCGCGTTC TACGCCACCT TGCGCAGCCC ACACCATTTG GCCCTGCCAG CTCCCTGCCC  
600

CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG  
660

CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC  
720

GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG  
780

CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCTTTTCC TCTACCAGGG GTCCTGCAG  
840

GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC  
900

GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG  
960

CAGCCCTAAT AA  
972

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 927 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC

240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT CTGCTTTCCA GCGCCGGGCA  
420

GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA  
480

CGCCACCTTG CGCAGCCCAC ACCATTGGGC CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG  
540

CTCAAGTCTT TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG  
600

CTGTGTGCCA CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG ACACTCTCTG  
660

GGCATCCCCCT GGGCTCCCCT GAGCTCCTGC CCCAGCCAGG CCCTGCAGCT GGCAGGCTGC  
720

TTGAGCCAAC TCCATAGCGG CCTTTTCCTC TACCAGGGGC TCCTGCAGGC CCTGGAAGGG  
780

ATATCCCCCG AGTTGGGTCC CACCTTGGAC ACACTGCAGC TGGACGTCGC CGACTTTGCC  
840

ACCACCATCT GGCAGCAGAT GGAAGAACTG GGAATGGCCC CTGCCCTGCA GCCCACCCAG  
900

GGTGCCATGC CGGCCTTCGC CTAATAA  
927

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA

180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTTCTGCT TTCCAGCGCC GGGCAGGAGG GGTCTTGTT  
480

GCTAGCCATC TGCAGAGCTT CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG  
540

CCCACACCAT TGGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG  
600

CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC  
660

AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT  
720

CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT  
780

AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCAGTTG  
840

GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG  
900

CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC  
960

TTCGCCTAAT AA  
972

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 963 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG

60

CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTAAT GGACAATAAC  
120

CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA  
180

GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CGCTAGCCAC GGCCGCACCC  
240

ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC  
300

TTCTATCTGA AAACCTTGGG GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC  
480

CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCTG  
540

TACCGCGTTC TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC  
600

CTGCTCAAGT CTTTAGAGCA AGTGAGAAAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG  
660

AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT  
720

CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC  
780

TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA  
840

GGGATATCCC CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT  
900

GCCACCACCA TCTGGCAGCA GATGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCTAA  
960

TAA  
963

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 972 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG  
60  
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAAAATAAC  
120  
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA  
180  
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC  
240  
ACGCGACATC CAATCATCAT CCGTGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC  
300  
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC  
360  
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420  
TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC  
480  
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCTG  
540  
TACCGCGTTC TACGCCACCT TGCGCAGCCC ACACCATTTG GCCCTGCCAG CTCCCTGCCC  
600  
CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG  
660  
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC  
720  
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG  
780  
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCTTTTCC TCTACCAGGG GCTCCTGCAG  
840  
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC  
900  
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG  
960  
CAGCCCTAAT AA  
972

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 963 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG  
60  
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAAAATAAC  
120  
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA  
180  
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC  
240  
ACGCGACATC CAATCATCAT CCGTGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC  
300  
TTCTATCTGA AAACCTTGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC  
360  
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420  
TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC  
480  
CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCTG  
540  
TACCGCGTTC TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC  
600  
CTGCTCAAGT CTTTAGAGCA AGTGAGAAAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG  
660  
AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT  
720  
CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC  
780  
TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA  
840  
GGGATATCCC CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT  
900  
GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCTAA  
960  
TAA  
963

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 972 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG  
60

CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTAAT GGACAATAAC  
120

CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA  
180

GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CGCTAGCCAC GGCCGCACCC  
240

ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC  
300

TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC  
480

CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCTG  
540

TACCGCGTTC TACGCCACCT TGCGCAGCCC ACACCATTTG GCCCTGCCAG CTCCCTGCCC  
600

CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA TGGCGCAGCG  
660

CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC  
720

GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG  
780

CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG  
840

GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC  
900

GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG  
960

CAGCCCTAAT AA  
972

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGA GGTTCACCCT TTGCCTACAC CTGTCCTGCT GCCTGCTGTG  
480

GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA CCAAGGCACA GGACATTCTG  
540

GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG ATGGCAGCAC GGGGACAACT GGGACCCACT  
600

TGCCTCTCAT CCCTCCTGGG GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG  
660

CAGAGCCTCC TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC  
720

AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT CCTGATGCTT  
780

GTAGGAGGGT CCACCTCTG CGTCAGGGAA TTCGGCGGCA ACATGGCGTC TCCCGCTCCG  
840

CCTGCTTG TG ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC  
900

AGACTGAGCC AGTGCCCA  
918

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 918 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGTT GCCTACACCT GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG  
480

GGAGAATGGA AAACCCAGAT GGAGGAGACC AAGGCACAGG ACATTCTGGG AGCAGTGACC  
540

CTTCTGCTGG AGGGAGTGAT GGCAGCACGG GGACAACTGG GACCCACTTG CCTCTCATCC  
600

CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT  
660

GGAACCCAGC TTCTCCACA GGCAGGACC ACAGCTCACA AGGATCCCAA TGCCATCTTC  
720

CTGAGCTTCC AACACCTGCT CCGAGGAAAG GTGCGTTTCC TGATGCTTGT AGGAGGGTCC  
780

ACCTCTGCG TCAGGGAATT CGGCGGCAAC ATGGCGTCTC CCGCTCCGCC TGCTTGTGAC  
840

CTCCGAGTCC TCAGTAAACT GCTTCGTGAC TCCCATGTCC TTCACAGCAG ACTGAGCCAG  
900

TGCCCAGAGG TTCACCT  
918

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGT CCTGCTGCCT GCTGTGGACT TTAGCTTGGG AGAATGGAAA  
480

ACCCAGATGG AGGAGACCAA GGCACAGGAC ATTCTGGGAG CAGTGACCCT TCTGCTGGAG  
540

GGAGTGATGG CAGCACGGGG ACAACTGGGA CCCACTTGCC TCTCATCCCT CCTGGGGCAG  
600

CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG GCCCTGCAGA GCCTCCTTGG AACCCAGCTT  
660

CCTCCACAGG GCAGGACCAC AGCTCACAAG GATCCCAATG CCATCTTCCT GAGCTTCCAA  
720

CACCTGCTCC GAGGAAAGGT GCGTTTCCTG ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC  
780

AGGGAATTCG GCGGCAACAT GCGTCTCCC GCTCCGCTG CTTGTGACCT CCGAGTCCTC  
840

AGTAAACTGC TTCGTGACTC CCATGTCCTT CACAGCAGAC TGAGCCAGTG CCCAGAGGTT  
900

CACCCTTTGC CTACACCT  
918

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACG TTC  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGC TGTGGACTTT AGCTTGGGAG AATGGAAAAAC CCAGATGGAG  
480

GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA  
540

GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG  
600

GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGA CCCAGCTTCC TCCACAGGGC  
660

AGGACCACAG CTCACAAGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA  
720

GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC  
780

GGCAACATGG CGTCTCCCGC TCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT  
840

CGTGACTCCC ATGTCCTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT  
900

ACACCTGTCC TGCTGCCT  
918

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 918 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC  
480

AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG  
540

GGACAACTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT  
600

CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC  
660

ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG  
720

GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGGAATT CGGCGGCAAC  
780

ATGGCGTCTC CCGCTCCGCC TGCTTGTGAC CTCCGAGTCC TCAGTAAACT GCTTCGTGAC  
840

TCCCATGTCC TTCACAGCAG ACTGAGCCAG TGCCCAGAGG TTCACCCTTT GCCTACACCT  
900

GTCTTGCTGC CTGCTGTG  
918

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 907 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCGGTTAC CCTTGAGCAA GCGCAGGAAC AACAGTACGT AGAGGGCGGT GGAGGCTCCC  
360

CGGGGAACCG TCTGGTCCAA TCTCTACTAT CAACCCGTCT CCTCCGTCTA AAGAATCTCA  
420

TAAACTCCAA ACATGGGAGA ATGGAAAACC CAGATGGAGG AGACCAAGGC ACAGGACATT  
480

CTGGAGCAGT GACCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA CTGGGACCCA  
540

CTTGCTCTCA TCCCTCCTGG GGCAGCTTTC TGGACAGGTC CGTCTCCTCC TTGGGGCCCT  
600

GCAGGCCTCC TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC  
660

AATGCATCTT CCTGAGCTTC CAACACCTGC TCCGAGGAAA GGTGCGTTTC CTGATGCTTG  
720

TAGGGGGTCC ACCCTCTGCG TCAGGGAATT CGGCGGCAAC ATGGCGTCTC CCGCTCCGCC  
780

TGCTGTGACC TCCGAGTCCT CAGTAAACTG CTCGTGACT CCCATGTCCT TCACAGCAGA  
840

CTGACCAGTG CCCAGAGGTT CACCCTTTGC CTACACCTGT CCTGCTGCCT GCTGTGGACT  
900

TTAGTTG  
907

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGG ACCCACTTGC CTCTCATCCC TCCTGGGGCA GCTTTCTGGA  
480

CAGGTCCGTC TCCTCCTTGG GGCCCTGCAG AGCCTCCTTG GAACCCAGCT TCCTCCACAG  
540

GGCAGGACCA CAGCTCACAA GGATCCCAAT GCCATCTTCC TGAGCTTCCA ACACCTGCTC  
600

CGAGGAAAGG TGCCTTTCCT GATGCTTGTA GGAGGGTCCA CCCTCTGCGT CAGGGAATTC  
660

GGCGGCAACA TGGCGTCTCC CGCTCCGCCT GCTTGTGACC TCCGAGTCCT CAGTAAACTG  
720

CTTCGTGACT CCCATGTCCT TCACAGCAGA CTGAGCCAGT GCCCAGAGGT TCACCCTTTG  
780

CCTACACCTG TCCTGCTGCC TGCTGTGGAC TTTAGCTTGG GAGAATGGAA AACCCAGATG  
840

GAGGAGACCA AGGCACAGGA CATTCTGGGA GCAGTGACCC TTCTGCTGGA GGGAGTGATG  
900

GCAGCACGGG GACAACTG  
918

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGG AACCCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG  
480

GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG  
540

ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCGGCAACAT GCGTCTCCC  
600

GCTCCGCCTG CTTGTGACCT CCGAGTCCTC AGTAAACTGC TTCGTGACTC CCATGTCCTT  
660

CACAGCAGAC TGAGCCAGTG CCCAGAGGTT CACCCTTTGC CTACACCTGT CCTGCTGCCT  
720

GCTGTGGACT TTAGCTTGGG AGAATGGAAA ACCCAGATGG AGGAGACCAA GGCACAGGAC  
780

ATTCTGGGAG CAGTGACCCT TCTGCTGGAG GGAGTGATGG CAGCACGGGG ACAACTGGGA  
840

CCCACTTG  
848

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGG CAGGACCACA GTCACAAGG ATCCCAATGC CATCTTCCTG  
480

AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG CGTTTCCTGA TGCTTGTAGG AGGGTCCACC  
540

CTCTGCGTCA GGGAATTCCG CGGCAACATG GCGTCTCCCG CTCCGCCTGC TTGTGACCTC  
600

CGAGTCCTCA GTAAACTGCT TCGTGACTCC CATGTCCTTC ACAGCAGACT GAGCCAGTGC  
660

CCAGAGGTTC ACCCTTTGCC TACACCTGTC CTGCTGCCTG CTGTGGACTT TAGCTTGGGA  
720

GAATGGAAAA CCCAGATGGA GGAGACCAAG GCACAGGACA TTCTGGGAGC AGTGACCCTT  
780

CTGCTGGAGG GAGTGATGGC AGCACGGGGA CAACTGGGAC CCACTTGCCT CTCATCCCTC  
840

CTGGGGCAGC TTTCTGGACA GGTCCGTCTC CTCCTTGGGG CCCTGCAGAG CCTCCTTGGA  
900

ACCCAGCTTC CTCCACAG  
918

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 918 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGC TCACAAGGAT CCCAATGCCA TCTTCCTGAG CTTCCAACAC  
480

CTGCTCCGAG GAAAGGTGCG TTTCTGATG CTTGTAGGAG GGTCCACCCT CTGCGTCAGG  
540

GAATTGCGCG GCAACATGGC GTCTCCCGCT CCGCCTGCTT GTGACCTCCG AGTCCTCAGT  
600

AAACTGCTTC GTGACTCCCA TGTCCCTTAC AGCAGACTGA GCCAGTGCCC AGAGGTTTAC  
660

CCTTTGCCTA CACCTGTCCT GCTGCCTGCT GTGGACTTTA GCTTGGGAGA ATGGAAAACC  
720

CAGATGGAGG AGACCAAGGC ACAGGACATT CTGGGAGCAG TGACCCTTCT GCTGGAGGGA  
780

GTGATGGCAG CACGGGGACA ACTGGGACCC ACTTGCCTCT CATCCCTCCT GGGGCAGCTT  
840

TCTGGACAGG TCCGTCTCCT CCTTGGGGCC CTGCAGAGCC TCCTTGGAAC CCAGCTTCCT  
900

CCACAGGGCA GGACCACA  
918

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 918 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTCTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA  
480

GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC  
540

GGCAACATGG CGTCTCCCGC TCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT  
600

CGTGACTCCC ATGTCCTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT  
660

ACACCTGTCC TGCTGCCTGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG  
720

GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA  
780

GCACGGGGAC AACTGGGACC CACTTGCCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG  
840

GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGA CCCAGCTTCC TCCACAGGGC  
900

AGGACCACAG CTCACAAG  
918

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGC CATCTTCCTG AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG  
480

CGTTTCCTGA TGCTTGTAGG AGGGTCCACC CTCTGCGTCA GGAATTCGG CGGCAACATG  
540

CGGTCTCCCG CTCCGCCTGC TTGTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC  
600

CATGTCCTTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC TACACCTGTC  
660

CTGCTGCCTG CTGTGGACTT TAGCTTGGGA GAATGGAAAA CCCAGATGGA GGAGACCAAG  
720

GCACAGGACA TTCTGGGAGC AGTGACCCTT CTGCTGGAGG GAGTGATGGC AGCACGGGGA  
780

CAACTGGGAC CCACTTGCCT CTCATCCCTC CTGGGGCAGC TTTCTGGACA GGTCCGTCTC  
840

CTCCTTGGGG CCCTGCAGAG CCTCCTTGA ACCCAGCTTC CTCCACAGGG CAGGACCACA  
900

GCTCACAAGG ATCCCAAT  
918

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGA GGTTCACCCT TTGCCTACAC CTGTCCTGCT GCCTGCTGTG  
480

GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA CCAAGGCACA GGACATTCTG  
540

GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG ATGGCAGCAC GGGGACAACT GGGACCCACT  
600

TGCCTCTCAT CCCTCCTGGG GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG  
660

CAGAGCCTCC TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC  
720

AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT CCTGATGCTT  
780

GTAGGAGGGT CCACCCTCTG CGTCAGGGAA TTCGGCAACA TGGCGTCTCC CGCTCCGCCT  
840

GCTTGTGACC TCCGAGTCCT CAGTAAACTG CTTGCTGACT CCCATGTCCT TCACAGCAGA  
900

CTGAGCCAGT GCCCA  
915

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 915 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTCTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGTT GCCTACACCT GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG  
480

GGAGAATGGA AAACCCAGAT GGAGGAGACC AAGGCACAGG ACATTCTGGG AGCAGTGACC  
540

CTTCTGCTGG AGGGAGTGAT GGCAGCACGG GGACAACTGG GACCCACTTG CCTCTCATCC  
600

CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT  
660

GGAACCCAGC TTCTCCACA GGCAGGACC ACAGCTCACA AGGATCCCAA TGCCATCTTC  
720

CTGAGCTTCC AACACCTGCT CCGAGGAAAAG GTGCGTTTCC TGATGCTTGT AGGAGGGTCC  
780

ACCCTCTGCG TCAGGGAATT CGGCAACATG GCGTCTCCCG CTCCGCCTGC TTGTGACCTC  
840

CGAGTCCTCA GTAAACTGCT TCGTGACTCC CATGTCCTTC ACAGCAGACT GAGCCAGTGC  
900

CCAGAGGTTC ACCCT  
915

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGT CCTGCTGCCT GCTGTGGACT TTAGCTTGGG AGAATGGAAA  
480

ACCCAGATGG AGGAGACCAA GGCACAGGAC ATTCTGGGAG CAGTGACCCT TCTGCTGGAG  
540

GGAGTGATGG CAGCACGGGG ACAACTGGGA CCCACTTGCC TCTCATCCCT CCTGGGGCAG  
600

CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG GCCCTGCAGA GCCTCCTTGG AACCCAGCTT  
660

CCTCCACAGG GCAGGACCAC AGCTCACAAG GATCCCAATG CCATCTTCCT GAGCTTCCAA  
720

CACCTGCTCC GAGGAAAGGT GCGTTTCCTG ATGCTTGTA GAGGGTCCAC CCTCTGCGTC  
780

AGGGAATTCG GCAACATGGC GTCTCCCGCT CCGCCTGCTT GTGACCTCCG AGTCCTCAGT  
840

AAACTGCTTC GTGACTCCCA TGTCCCTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTTAC  
900

CCTTTGCCTA CACCT  
915

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60  
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120  
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180  
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT  
240  
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC  
300  
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360  
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420  
CATAAATCTC CAAACATGGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG  
480  
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA  
540  
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG  
600  
GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGAA CCCAGCTTCC TCCACAGGGC  
660  
AGGACCACAG CTCACAAGGA TCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA  
720  
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC  
780  
AACATGGCGT CTCCCGCTCC GCCTGCTTGT GACCTCCGAG TCCTCAGTAA ACTGCTTCGT  
840  
GACTCCCATG TCCTTCACAG CAGACTGAGC CAGTGCCCAG AGGTTACCC TTTGCCTACA  
900  
CCTGTCCTGC TGCCT  
915

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60  
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120  
CGACTTCCAA ACCTGGAGAG CTTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180  
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240  
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300  
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360  
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420  
CATAAATCTC CAAACATGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC  
480  
AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG  
540  
GGACAACCTG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT  
600  
CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC  
660  
ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG  
720  
GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGGAATT CGGCAACATG  
780  
GCGTCTCCCG CTCCGCCTGC TTGTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC  
840  
CATGTCCTTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC TACACCTGTC  
900  
CTGCTGCCTG CTGTG  
915

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 915 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGG AGAATGGAAA ACCCAGATGG AGGAGACCAA GGCACAGGAC  
480

ATTCTGGGAG CAGTGACCCT TCTGCTGGAG GGAGTGATGG CAGCACGGGG ACAACTGGGA  
540

CCCACTTGCC TCTCATCCCT CCTGGGGCAG CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG  
600

GCCCTGCAGA GCCTCCTTGG AACCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG  
660

GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG  
720

ATGCTTGTA GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCAACATGGC GTCTCCCGCT  
780

CCGCTGCTT GTGACCTCCG AGTCCTCAGT AAAGTCTTC GTGACTCCCA TGTCTTCAC  
840

AGCAGACTGA GCCAGTGCCC AGAGGTTTAC CCTTTGCCTA CACCTGTCCT GCTGCCTGCT  
900

GTGGACTTTA GCTTG  
915

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 915 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60  
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120  
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180  
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240  
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300  
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360  
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420  
CATAAATCTC CAAACATGGG ACCCACTTGC CTCTCATCCC TCCTGGGGCA GCTTTCTGGA  
480  
CAGGTCCGTC TCCTCCTTGG GGCCCTGCAG AGCCTCCTTG GAACCCAGCT TCCTCCACAG  
540  
GGCAGGACCA CAGCTCACAA GGATCCCAAT GCCATCTTCC TGAGCTTCCA ACACCTGCTC  
600  
CGAGGAAAGG TGCGTTTCCT GATGCTTGTA GGAGGGTCCA CCCTCTGCGT CAGGGAATTC  
660  
GGCAACATGG CGTCTCCCGC TCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT  
720  
CGTGACTCCC ATGTCCTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT  
780  
ACACCTGTCC TGCTGCCTGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG  
840  
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA  
900  
GCACGGGGAC AACTG  
915

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGG AACCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG  
480

GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG  
540

ATGCTTGTA GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCAACATGGC GTCTCCCGCT  
600

CCGCCTGCTT GTGACCTCCG AGTCCTCAGT AAAGTCTTTC GTGACTCCCA TGTCTTCAC  
660

AGCAGACTGA GCCAGTGCCC AGAGGTTTAC CCTTTGCCTA CACCTGTCCT GCTGCCTGCT  
720

GTGGACTTTA GCTTGGGAGA ATGGAAAACC CAGATGGAGG AGACCAAGGC ACAGGACATT  
780

CTGGGAGCAG TGACCTTCT GCTGGAGGGA GTGATGGCAG CACGGGGACA ACTGGGACCC  
840

ACTTGCTCT CATCCCTCCT GGGGCAGCTT TCTGGACAGG TCCGTCTCCT CCTTGGGGCC  
900

CTGCAGAGCC TCCTT  
915

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGG CAGGACCACA GCTCACAAGG ATCCCAATGC CATCTTCCTG  
480

AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG CGTTTCCTGA TGCTTGTAGG AGGGTCCACC  
540

CTCTGCGTCA GGAATTTCGG CAACATGGCG TCTCCCGCTC CGCCTGCTTG TGACCTCCGA  
600

GTCTTCAGTA AACTGCTTCG TGAATCCCAT GTCCTTCACA GCAGACTGAG CCAGTGCCCA  
660

GAGGTTACAC CTTTGCCTAC ACCTGTCCTG CTGCCTGCTG TGGACTTTAG CTTGGGAGAA  
720

TGGAAAACCC AGATGGAGGA GACCAAGGCA CAGGACATTC TGGGAGCAGT GACCCCTCTG  
780

CTGGAGGGAG TGATGGCAGC ACGGGGACAA CTGGGACCCA CTTGCCTCTC ATCCCTCCTG  
840

GGGCAGCTTT CTGGACAGGT CCGTCTCCTC CTTGGGGCCC TGCAGAGCCT CCTTGGAAACC  
900

CAGCTTCCTC CACAG  
915

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGC TCACAAGGAT CCAATGCCA TCTTCCTGAG CTTCCAACAC  
480

CTGCTCCGAG GAAAGGTGCG TTTCCTGATG CTTGTAGGAG GGTCCACCCT CTGCGTCAGG  
540

GAATTCGGCA ACATGGCGTC TCCCGCTCCG CCTGCTTGTC ACCTCCGAGT CCTCAGTAAA  
600

CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGAGCC AGTGCCCAGA GGTTCACCCT  
660

TTGCCTACAC CTGTCCTGCT GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG  
720

ATGGAGGAGA CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG  
780

ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG GCAGCTTTCT  
840

GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC TTGGAACCCA GCTTCCTCCA  
900

CAGGGCAGGA CCACA  
915

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 915 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTCTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA  
480

GGAAAAGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC  
540

AACATGGCGT CTCCCGCTCC GCCTGCTTGT GACCTCCGAG TCCTCAGTAA ACTGCTTCGT  
600

GACTCCCATG TCCTTCACAG CAGACTGAGC CAGTGCCCAG AGGTTACCC TTTGCCTACA  
660

CCTGTCTGCTG TGCCTGCTGT GGACTTTAGC TTGGGAGAAT GGAAAACCCA GATGGAGGAG  
720

ACCAAGGCAC AGGACATTCT GGGAGCAGTG ACCCTTCTGC TGGAGGGAGT GATGGCAGCA  
780

CGGGGACAAC TGGGACCCAC TTGCCTCTCA TCCCTCCTGG GGCAGCTTTC TGGACAGGTC  
840

CGTCTCCTCC TTGGGGCCCT GCAGAGCCTC CTTGGAACCC AGCTTCCTCC ACAGGGCAGG  
900

ACCACAGCTC ACAAG  
915

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGC CATCTTCCTG AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG  
480

CGTTTCCTGA TGCTTGTAGG AGGGTCCACC CTCTGCGTCA GGAATTCGG CAACATGGCG  
540

TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGAATCCCAT  
600

GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACC CTTGCCTAC ACCTGTCCTG  
660

CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA  
720

CAGGACATTC TGGGAGCAGT GACCCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA  
780

CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC  
840

CTTGGGGCCC TGCAGAGCCT CCTTGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT  
900

CACAAGGATC CCAAT  
915

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

GACTTCCAAA CCTGGAGAGC TTCGTAAGGG CTGTCAAGAA CTTAGAAAAT GCATCAGGTA  
180

TGAGGCAATT CTTCGTAATC TCCAACCATG TCTGCCCTCT GCCACGGCCG CACCCTCTCG  
240

CATCCAATCA TCATCAAGGC AGGTGACTGG CAAGAATTCC GGGAAAAACT GACGTTCTAT  
300

TGGTTACCTT TGAGCAAGCG CAGGAACAAC AGTACGTAGA GGGCGGTGGA GGCTCCCCGG  
360

TAACCGTCTG GTCCAATCTC TACTATCAAC CCGTCTCCTC CGTCTAAAGA ATCTCATAAA  
420

TCTCCAAACA TGGAGGTTCA CCCTTTGCCT ACACCTGTCC TGCTGCCTGC TGTGGACTTT  
480

AGCTTGGGAG AATGGAAAAC CCAGATGGAG GAGACCAAGG CACAGGACAT TCTGGGAGCA  
540

GTGACCCCTT TGCTGGAGGG AGTGATGGCA GCACGGGGAC AACTGGGACC CACTTGCCTC  
600

TCATCCCTCC TGGGGCAGCT TTCTGGACAG GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC  
660

CTCCTTGGA CCCAGCTTCC TCCACAGGGC AGGACCACAG CTCACAAGGA TCCCAATGCC  
720

ATCTTCCTGA GCTTCCAACA CCTGCTCCGA GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA  
780

GGGTCCACCC TCTGCGTCAG GGAATTCGGC GGCAACGGCG GCAACATGGC GTCCCCAGCG  
840

CCGCCTGCTT GTGACCTCCG AGTCCTCAGT AAAGTCTTC GTGACTCCCA TGTCTTCAC  
900

AGCAGACTGA GCCAGTGCCC A  
921

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 927 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGTT GCCTACACCT GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG  
480

GGAGAATGGA AAACCCAGAT GGAGGAGACC AAGGCACAGG ACATTCTGGG AGCAGTGACC  
540

CTTCTGCTGG AGGGAGTGAT GGCAGCACGG GGACAACTGG GACCCACTTG CCTCTCATCC  
600

CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT  
660

GGAACCCAGC TTCCTCCACA GGGCAGGACC ACAGCTCACA AGGATCCCAA TGCCATCTTC  
720

CTGAGCTTCC AACACCTGCT CCGAGGAAAG GTGCGTTTCC TGATGCTTGT AGGAGGGTCC  
780

ACCCTCTGCG TCAGGGAATT CGGCGGCAAC GGC GGCAACA TGGCGTCCCC AGCGCCGCCT  
840

GCTTGTGACC TCCGAGTCCT CAGTAACTG CTCGTGACT CCCATGTCCT TCACAGCAGA  
900

CTGAGCCAGT GCCCAGAGGT TCACCCT  
927

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGT CCTGCTGCCT GCTGTGGACT TTAGCTTGGG AGAATGGAAA  
480

ACCCAGATGG AGGAGACCAA GGCACAGGAC ATTCTGGGAG CAGTGACCCT TCTGCTGGAG  
540

GGAGTGATGG CAGCACGGGG ACAACTGGGA CCCACTTGCC TCTCATCCCT CCTGGGGCAG  
600

CTTCTGGAC AGGTCCGTCT CCTCCTTGGG GCCCTGCAGA GCCTCCTTGG AACCCAGCTT  
660

CCTCCACAGG GCAGGACCAC AGCTCACAAG GATCCCAATG CCATCTTCCT GAGCTTCCAA  
720

CACCTGCTCC GAGGAAAGGT GCGTTTCCTG ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC  
780

AGGGAATTCG GCGGCAACGG CGGCAACATG GCGTCCCCAG CGCCGCCTGC TTGTGACCTC  
840

CGAGTCCTCA GTAAACTGCT TCGTGACTCC CATGTCCTTC ACAGCAGACT GAGCCAGTGC  
900

CCAGAGGTTC ACCCTTTGCC TACACCT  
927

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG  
480

GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA  
540

GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG  
600

GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGA CCCAGCTTCC TCCACAGGGC  
660

AGGACCACAG CTCACAAGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA  
720

GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC  
780

GGCAACGGCG GCAACATGGC GTCCCCAGCG CCGCCTGCTT GTGACCTCCG AGTCCTCAGT  
840

AAACTGCTTC GTGACTCCCA TGTCCCTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTTAC  
900

CCTTTGCCTA CACCTGTCCT GCTGCCT  
927

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC  
480

AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG  
540

GGACAACCTG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT  
600

CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGCAGGACC  
660

ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG  
720

GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGGAATT CGGCGGCAAC  
780

GGCGGCAACA TGGCGTCCCC AGCGCCGCCT GCTTGTGACC TCCGAGTCCT CAGTAAACTG  
840

CTTCGTGACT CCCATGTCCT TCACAGCAGA CTGAGCCAGT GCCCAGAGGT TCACCCTTTG  
900

CCTACACCTG TCCTGCTGCC TGCTGTG  
927

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGG AGAATGGAAA ACCCAGATGG AGGAGACCAA GGCACAGGAC  
480

ATTCTGGGAG CAGTGACCCT TCTGCTGGAG GGAGTGATGG CAGCACGGGG ACAACTGGGA  
540

CCCACTTGCC TCTCATCCCT CCTGGGGCAG CTTTCTGGAC AGGTCCGTCT CCTCCTTGGG  
600

GCCCTGCAGA GCCTCCTTGG AACCCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG  
660

GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG  
720

ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCGGCAACGG CGGCAACATG  
780

GCGTCCCCAG CGCCGCCTGC TTGTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC  
840

CATGTCCTTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC TACACCTGTC  
900

CTGCTGCCTG CTGTGGACTT TAGCTTG  
927

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGG ACCCACTTGC CTCTCATCCC TCCTGGGGCA GCTTTCTGGA  
480

CAGGTCCGTC TCCTCCTTGG GGCCCTGCAG AGCCTCCTTG GAACCCAGCT TCCTCCACAG  
540

GGCAGGACCA CAGCTCACAA GGATCCCAAT GCCATCTTCC TGAGCTTCCA ACACCTGCTC  
600

CGAGGAAAGG TGC GTTTTCCT GATGCTTGTA GGAGGGTCCA CCCTCTGCGT CAGGGAATTC  
660

GGCGGCAACG GCGGCAACAT GGCGTCCCCA GCGCCGCTG CTTGTGACCT CCGAGTCCTC  
720

AGTAAACTGC TTCGTGACTC CCATGTCCTT CACAGCAGAC TGAGCCAGTG CCCAGAGGTT  
780

CACCCTTTGC CTACACCTGT CCTGCTGCCT GCTGTGGACT TTAGCTTGGG AGAATGGAAA  
840

ACCCAGATGG AGGAGACCAA GGCACAGGAC ATTCTGGGAG CAGTGACCCT TCTGCTGGAG  
900

GGAGTGATGG CAGCACGGGG ACAACTG  
927

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGG AACCCAGCTT CCTCCACAGG GCAGGACCAC AGCTCACAAG  
480

GATCCCAATG CCATCTTCCT GAGCTTCCAA CACCTGCTCC GAGGAAAGGT GCGTTTCCTG  
540

ATGCTTGTAG GAGGGTCCAC CCTCTGCGTC AGGGAATTCG GCGGCAACGG CGGCAACATG  
600

GCGTCCCCAG CGCCGCCTGC TTGTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC  
660

CATGTCCCTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC TACACCTGTC  
720

CTGCTGCCTG CTGTGGACTT TAGCTTGGGA GAATGGAAAA CCCAGATGGA GGAGACCAAG  
780

GCACAGGACA TTCTGGGAGC AGTGACCCTT CTGCTGGAGG GAGTGATGGC AGCACGGGGA  
840

CAACTGGGAC CCACTTGCCT CTCATCCCTC CTGGGGCAGC TTTCTGGACA GGTCCGTCTC  
900

CTCCTTGGGG CCCTGCAGAG CCTCCTT  
927

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTT  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGG CAGGACCACA GCTCACAAGG ATCCCAATGC CATCTTCCTG  
480

AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG CGTTTCCTGA TGCTTGTAGG AGGGTCCACC  
540

CTCTGCGTCA GGAATTCGG CGGCAACGGC GGCAACATGG CGTCCCCAGC GCCGCCTGCT  
600

TGTGACCTCC GAGTCCTCAG TAAACTGCTT CGTGACTCCC ATGTCCTTCA CAGCAGACTG  
660

AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT ACACCTGTCC TGCTGCCTGC TGTGGACTTT  
720

AGCTTGGGAG AATGGAAAAC CCAGATGGAG GAGACCAAGG CACAGGACAT TCTGGGAGCA  
780

GTGACCCTTC TGCTGGAGGG AGTGATGGCA GCACGGGGAC AACTGGGACC CACTTGCCTC  
840

TCATCCCTCC TGGGGCAGCT TTCTGGACAG GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC  
900

CTCCTTGGA CCCAGCTTCC TCCACAG  
927

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120

CGACTTCCAA ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTC  
300

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420

CATAAATCTC CAAACATGGC TCACAAGGAT CCAATGCCA TCTTCCTGAG CTTCCAACAC  
480

CTGCTCCGAG GAAAGGTGCG TTTCTGATG CTTGTAGGAG GGTCCACCCT CTGCGTCAGG  
540

GAATTCGGCG GCAACGGCGG CAACATGGCG TCCCCAGCGC CGCCTGCTTG TGACCTCCGA  
600

GTCCTCAGTA AACTGCTTCG TGACTCCCAT GTCCTTCACA GCAGACTGAG CCAGTGCCCA  
660

GAGGTTCAAC CTTTGCCTAC ACCTGTCCTG CTGCCTGCTG TGGACTTTAG CTTGGGAGAA  
720

TGGAAAACCC AGATGGAGGA GACCAAGGCA CAGGACATTC TGGGAGCAGT GACCCTTCTG  
780

CTGGAGGGAG TGATGGCAGC ACGGGGACAA CTGGGACCCA CTTGCCTCTC ATCCCTCCTG  
840

GGGCAGCTTT CTGGACAGGT CCGTCTCCTC CTTGGGGCCC TGCAGAGCCT CCTTGAACC  
900

CAGCTTCCTC CACAGGGCAG GACCACA  
927

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
 60  
 TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
 120  
 CGACTTCCAA ACCTGGAGAG CTTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
 180  
 ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
 240  
 CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTT  
 300  
 TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
 360  
 CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
 420  
 CATAAATCTC CAAACATGGA TCCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA  
 480  
 GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC  
 540  
 GGCAACGGCG GCAACATGGC GTCCCCAGCG CCGCCTGCTT GTGACCTCCG AGTCCTCAGT  
 600  
 AAACTGCTTC GTGACTCCCA TGTCCCTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTTAC  
 660  
 CCTTTGCCTA CACCTGTCCT GCTGCCTGCT GTGGACTTTA GCTTGGGAGA ATGGAAAACC  
 720  
 CAGATGGAGG AGACCAAGGC ACAGGACATT CTGGGAGCAG TGACCCCTTCT GCTGGAGGGA  
 780  
 GTGATGGCAG CACGGGGACA ACTGGGACCC ACTTGCCTCT CATCCCTCCT GGGGCAGCTT  
 840  
 TCTGGACAGG TCCGTCTCCT CCTTGGGGCC CTGCAGAGCC TCCTTGAAC CCAGCTTCCT  
 900  
 CCACAGGGCA GGACCACAGC TCACAAG  
 927

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60  
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120  
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180  
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT  
240  
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC  
300  
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360  
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420  
CATAAATCTC CAAACATGGC CATCTTCCTG AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG  
480  
CGTTTCCTGA TGCTTGTAGG AGGGTCCACC CTCTGCGTCA GGAATTCGG CGGCAACGGC  
540  
GGCAACATGG CGTCCCCAGC GCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT  
600  
CGTGACTCCC ATGTCCTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT  
660  
ACACCTGTCC TGCTGCCTGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG  
720  
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCCTT TGCTGGAGGG AGTGATGGCA  
780  
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG  
840  
GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGAA CCCAGCTTCC TCCACAGGGC  
900  
AGGACCACAG CTCACAAGGA TCCCAAT  
927

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
60  
TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT  
120  
CGACTTCCAA ACCTGGAGAG CTTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
180  
ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
240  
CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTC  
300  
TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
360  
CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
420  
CATAAATCTC CAAACATGGA TCCAATGCC ATCTTCCTGA GCTTCCAACA CCTGCTCCGA  
480  
GGAAAGGTGC GTTTCCTGAT GCTTGTAGGA GGGTCCACCC TCTGCGTCAG GGAATTCGGC  
540  
GGCAACATGG CGTCTCCCGC TCCGCCTGCT TGTGACCTCC GAGTCCTCAG TAAACTGCTT  
600  
CGTGACTCCC ATGTCCTTCA CAGCAGACTG AGCCAGTGCC CAGAGGTTCA CCCTTTGCCT  
660  
ACACCTGTCC TGCTGCCTGC TGTGGACTTT AGCTTGGGAG AATGGAAAAC CCAGATGGAG  
720  
GAGACCAAGG CACAGGACAT TCTGGGAGCA GTGACCCTTC TGCTGGAGGG AGTGATGGCA  
780  
GCACGGGGAC AACTGGGACC CACTTGCCTC TCATCCCTCC TGGGGCAGCT TTCTGGACAG  
840  
GTCCGTCTCC TCCTTGGGGC CCTGCAGAGC CTCCTTGGAA CCCAGGGCAG GACCACAGCT  
900  
CACAAG  
906

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 993 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60  
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
120  
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180  
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240  
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300  
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360  
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420  
TCTCATAAAT CTCCAAACAT GTCTTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC  
480  
GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG  
540  
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GTCCTGCAG  
600  
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC  
660  
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG  
720  
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG  
780  
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC  
840  
CTTGCGCAGC CCGGCGGCGG CTCTGACATG GCTACACCAT TAGGCCCTGC CAGCTCCCTG  
900  
CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGGA AGATCCAGGG CGATGGCGCA  
960  
GCGCTCCAGG AGAAGCTGTG TGCCACCTAA TAA  
993

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 993 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA
60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC
120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA
180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC
240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC
360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA
420
TCTCATAAAT CTCCAAACAT GTCTCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG
480
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCCT
540
GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA
600
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA
660
CGCCACCTTG CGCAGCCCGG CGGCGGCTCT GACATGGCTA CACCATTAGG CCCTGCCAGC
720
TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT
780
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG
840
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG
900
GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG
```

960

CTCCTGCAGG CCCTGGAAGG GATATCCTAA TAA  
993

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GTCTTCTGCT TTCCAGCGCC GGGCAGGAGG GGTCTTGGTT  
480

GCTAGCCATC TGCAGAGCTT CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG  
540

CCCGGCGGCG GCTCTGACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC  
600

TTCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG  
660

GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC  
720

TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA  
780

GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCTCTACC AGGGGCTCCT GCAGGCCCTG

840

GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC  
900

TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC CCTGCAGCCC  
960

ACCCAGGGTG CCATGCCGGC CTTCGCCTAA TAA  
993

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GTCTATGGCC CCTGCCCTGC AGCCCACCCA GGGTGCCATG  
480

CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG  
540

CAGAGCTTCC TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CGGCGGCGGC  
600

TCTGACATGG CTACACCATT AGGCCCTGCC AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG  
660

TCTTTAGAGC AAGTGAGGAA GATCCAGGGC GATGGCGCAG CGCTCCAGGA GAAGCTGTGT

720

GCCACCTACA AGCTGTGCCA CCCCAGAGGAG CTGGTGCTGC TCGGACACTC TCTGGGCATC  
780

CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC  
840

CAACTCCATA GCGGCCTTTT CCTCTACCAG GGGCTCCTGC AGGCCCTGGA AGGGATATCC  
900

CCCAGATTGG GTCCACCTT GGACACACTG CAGCTGGACG TCGCCGACTT TGCCACCACC  
960

ATCTGGCAGC AGATGGAAGA ACTGGGATAA TAA  
993

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GTCTACCCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC  
480

CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCTG  
540

TACCGCGTTC TACGCCACCT TGCGCAGCCC GGCGGCGGCT CTGACATGGC TACACCATTA

600

GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG  
660

ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC  
720

CCCGAGGAGC TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC  
780

TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG CGGCCTTTTC  
840

CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC CCGAGTTGGG TCCCACCTTG  
900

GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA GATGGAAGAA  
960

CTGGGAATGG CCCCTGCCCT GCAGCCCTAA TAA  
993

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ATGGCTACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA  
60

GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC  
120

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG  
180

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC  
240

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCGAG  
300

TTGGGTCCCA CCTTGACAC ACTGCAGCTG GACGTGCGCG ACTTTGCCAC CACCATCTGG  
360

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG  
420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG

480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCGG CGGCGGCTCT  
540

GACATGGCTA CACCATTGGG CCCTGCCAGC TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT  
600

TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC  
660

ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG GACACTCTCT GGGCATCCCC  
720

TGGGCTCCCC TGAGCTCCTG CCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA  
780

CTCCATAGCG GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCCCC  
840

GAGTTGGGTC CCACCTTGA CACACTGCAG CTGGACGTCG CCGACTTTGC CACCACCATC  
900

TGGCAGCAGA TGAAGAAGT GGGAATGGCC CCTGCCCTGC AGCCCACCCA TCCTGGTTGC  
960

TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC  
1020

CTGATAA  
1027

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 155 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln |
|     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Gly | Asn | Met | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu  
 165 170 175  
 Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val  
 180 185 190  
 His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu  
 195 200 205  
 Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu  
 210 215 220  
 Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln  
 225 230 235 240  
 Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln  
 245 250 255  
 Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Gly  
 260 265 270  
 Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln  
 275 280 285  
 His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser  
 290 295 300  
 Thr Leu Cys Val Arg  
 305

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu  
 1 5 10 15  
 Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val  
 20 25 30  
 His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu  
 35 40 45  
 Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu  
 50 55 60  
 Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln  
 65 70 75 80  
 Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln

| 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Asn | Met | Ala | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu | Arg |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | His |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln | Val |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln |  |  |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |  |
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  | .   |  |  |
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Gly | Asn | Met | Ala |  |  |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln |  |  |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg |     |     |     |     |     |     |     |  |  |
|     | 305 |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu | 1   | 5   | 10  | 15  |
| Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | 20  | 25  | 30  |     |
| His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu | 35  | 40  | 45  |     |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | 50  | 55  | 60  |     |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln | 65  | 70  | 75  | 80  |
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln | 85  | 90  | 95  |     |
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu | 100 | 105 | 110 |     |
| Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe | 115 | 120 | 125 |     |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu | 130 | 135 | 140 |     |
| Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Gly | Asn | Gly | Gly | 145 | 150 | 155 | 160 |
| Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | 165 | 170 | 175 |     |
| Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | 180 | 185 | 190 |     |
| Pro | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | 195 | 200 | 205 |     |
| Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | 210 | 215 | 220 |     |
| Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | 225 | 230 | 235 | 240 |
| Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | 245 | 250 | 255 |     |
| Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly |     |     |     |     |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 260                                                             | 265 | 270 |
| Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn |     |     |
| 275                                                             | 280 | 285 |
| Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe |     |     |
| 290                                                             | 295 | 300 |
| Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg                 |     |     |
| 305                                                             | 310 | 315 |

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 302 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

|                                                                 |             |
|-----------------------------------------------------------------|-------------|
| Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro |             |
| 1                                                               | 5 10 15     |
| Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser |             |
| 20                                                              | 25 30       |
| Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val |             |
| 35                                                              | 40 45       |
| Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu |             |
| 50                                                              | 55 60       |
| Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg |             |
| 65                                                              | 70 75 80    |
| His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys |             |
| 85                                                              | 90 95       |
| Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Tyr     |             |
| 100                                                             | 105 110     |
| Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly Gly Ser |             |
| 115                                                             | 120 125     |
| Asn Met Ala Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly |             |
| 130                                                             | 135 140     |
| His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln |             |
| 145                                                             | 150 155 160 |
| Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe |             |
| 165                                                             | 170 175     |
| Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu |             |
| 180                                                             | 185 190     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | Asn | 130 | 135 | 140 |
| Met | Ala | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | 145 | 150 | 155 |
| Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | 165 | 170 | 175 |
| Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | 180 | 185 | 190 |
| Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly | 195 | 200 | 205 |
| Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr | 210 | 215 | 220 |
| Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro | 225 | 230 | 235 |
| Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | 245 | 250 | 255 |
| Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | 260 | 265 | 270 |
| Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Ser | Gly | Gly | Ser | Gly | Gly | 275 | 280 | 285 |
| Ser | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | 290 | 295 | 300 |
| Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr |     |     |     | 305 | 310 | 315 |

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 302 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |    |    |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro | 1  | 5  | 10 | 15 |
| Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser | 20 | 25 | 30 |    |
| Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val | 35 | 40 | 45 |    |
| Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu |    |    |    |    |

| 50  |     | 55  |     | 60  |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|
| Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg |  |  |  |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |  |  |  |
| His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys |  |  |  |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |  |  |
| Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Tyr |  |  |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |  |  |  |  |
| Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser |  |  |  |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |  |
| Asn | Met | Ala | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp |  |  |  |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |  |  |
| Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly |  |  |  |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |  |
| Met | Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala |  |  |  |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |  |  |  |
| Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu |  |  |  |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |  |  |  |
| Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln |  |  |  |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |  |
| Pro | Ser | Gly | Gly | Ser | Gly | Gly | Ser | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu |  |  |  |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |  |  |
| Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys |  |  |  |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |  |  |  |
| Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu |  |  |  |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |  |  |  |
| Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser |  |  |  |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |  |  |  |
| Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu |  |  |  |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |  |  |
| Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser |     |     |  |  |  |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Tyr |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | Ser |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | Asn |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Met | Ala | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val |  |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |  |  |
| Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met |  |  |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |  |  |
| Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln |  |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |  |
| Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Ser | Gly | Gly | Ser | Gly | Gly | Ser | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser |     |     |     |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Tyr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Asn | Met | Ala | Met | Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Leu | Ala | Gln | Pro | Ser | Gly | Gly | Ser | Gly | Gly | Ser | Gln | Ser | Phe | Leu | Leu |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His |  |

|                                                                 |     |  |     |  |     |
|-----------------------------------------------------------------|-----|--|-----|--|-----|
|                                                                 | 245 |  | 250 |  | 255 |
| Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile | 260 |  | 265 |  | 270 |
| Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala | 275 |  | 280 |  | 285 |
| Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly         | 290 |  | 295 |  | 300 |

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 317 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro | 1   | 5   | 10  | 15  |
| Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser | 20  | 25  | 30  |     |
| Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val | 35  | 40  | 45  |     |
| Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu | 50  | 55  | 60  |     |
| Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg | 65  | 70  | 75  | 80  |
| His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys | 85  | 90  | 95  |     |
| Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Tyr     | 100 | 105 | 110 |     |
| Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser | 115 | 120 | 125 |     |
| Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn | 130 | 135 | 140 |     |
| Met Ala Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala | 145 | 150 | 155 | 160 |
| Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser | 165 | 170 | 175 |     |
| His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu | 180 | 185 | 190 |     |

Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys  
195 200 205

Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln  
210 215 220

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val  
225 230 235 240

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys  
245 250 255

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
260 265 270

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser  
275 280 285

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp  
290 295 300

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly  
305 310 315

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 302 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro  
1 5 10 15

Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser  
20 25 30

Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val  
35 40 45

Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu  
50 55 60

Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg  
65 70 75 80

His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys  
85 90 95

Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Tyr  
100 105 110

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser |  |  |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |
| Asn | Met | Ala | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln |  |  |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |  |
| Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe | Leu |  |  |  |  |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |
| Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Ser | Gly | Gly |  |  |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |  |  |  |
| Ser | Gly | Gly | Ser | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg |  |  |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |  |  |
| Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr |  |  |  |  |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |
| Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | Ser | Leu |  |  |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |  |
| Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln |  |  |  |  |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |  |  |
| Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln |  |  |  |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |  |  |
| Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr |  |  |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |  |  |
| Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp |  |  |  |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |  |
| Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro |     |     |  |  |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro |  |  |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |  |  |
| Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser |  |  |  |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |  |  |  |
| Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val |  |  |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |  |  |
| Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu |  |  |  |  |

| 50                                                              | 55  | 60          |
|-----------------------------------------------------------------|-----|-------------|
| Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg |     |             |
| 65                                                              | 70  | 75 80       |
| His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys |     |             |
|                                                                 | 85  | 90 95       |
| Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Tyr |     |             |
|                                                                 | 100 | 105 110     |
| Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser |     |             |
|                                                                 | 115 | 120 125     |
| Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn |     |             |
|                                                                 | 130 | 135 140     |
| Met Ala Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg |     |             |
|                                                                 | 145 | 150 155 160 |
| Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu |     |             |
|                                                                 | 165 | 170 175     |
| Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly Ser |     |             |
|                                                                 | 180 | 185 190     |
| Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys |     |             |
|                                                                 | 195 | 200 205     |
| Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr |     |             |
|                                                                 | 210 | 215 220     |
| Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly |     |             |
|                                                                 | 225 | 230 235 240 |
| Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu |     |             |
|                                                                 | 245 | 250 255     |
| Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly |     |             |
|                                                                 | 260 | 265 270     |
| Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu |     |             |
|                                                                 | 275 | 280 285     |
| Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln |     |             |
|                                                                 | 290 | 295 300     |
| Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro             |     |             |
|                                                                 | 305 | 310 315     |

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |  |
| Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Tyr |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Asn | Met | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Leu | Ala | Gln | Pro | Ser | Gly | Gly | Ser | Gly | Gly | Ser | Gln | Ser | Phe | Leu | Leu |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala |     |     |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 317 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Tyr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | Ser |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | Asn |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Met | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ala | Gln | Pro | Ser | Gly | Gly | Ser | Gly | Gly | Ser | Gln | Ser | Phe | Leu | Leu | Lys |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 245 |     | 250 |     | 255 |     |     |     |     |     |     |     |     |     |     |
| Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser |
|     | 260 |     | 265 |     | 270 |     |     |     |     |     |     |     |     |     |     |
| Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp |
|     | 275 |     | 280 |     | 285 |     |     |     |     |     |     |     |     |     |     |
| Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro |
|     | 290 |     | 295 |     | 300 |     |     |     |     |     |     |     |     |     |     |
| Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala |     |     |     |
|     | 305 |     | 310 |     | 315 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Tyr |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Asn | Met | Ala | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     |     | 175 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | 180 | 185 | 190 |
| Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | 195 | 200 | 205 |
| Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln | 210 | 215 | 220 |
| Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg | Arg | 225 | 230 | 235 |
| Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | 245 | 250 | 255 |
| Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Thr | Pro | Leu | Gly | Pro | 260 | 265 | 270 |
| Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | 275 | 280 | 285 |
| Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | 290 | 295 | 300 |
| Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 305 |     |     |

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |    |    |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro | 1  | 5  | 10 | 15 |
| Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser | 20 | 25 | 30 |    |
| Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val | 35 | 40 | 45 |    |
| Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu | 50 | 55 | 60 |    |
| Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg | 65 | 70 | 75 | 80 |
| His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys | 85 | 90 | 95 |    |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Leu        | Thr        | Phe        | Tyr<br>100 | Leu        | Val        | Thr        | Leu        | Glu<br>105 | Gln        | Ala        | Gln        | Glu        | Gln<br>110 | Gln        | Tyr        |
| Val        | Glu        | Gly<br>115 | Gly        | Gly        | Gly        | Ser        | Pro<br>120 | Gly        | Glu        | Pro        | Ser        | Gly<br>125 | Pro        | Ile        | Ser        |
| Thr        | Ile<br>130 | Asn        | Pro        | Ser        | Pro        | Pro<br>135 | Ser        | Lys        | Glu        | Ser        | His<br>140 | Lys        | Ser        | Pro        | Asn        |
| Met<br>145 | Ala        | Tyr        | Lys        | Leu        | Cys<br>150 | His        | Pro        | Glu        | Glu        | Leu<br>155 | Val        | Leu        | Leu        | Gly        | His<br>160 |
| Ser        | Leu        | Gly        | Ile        | Pro<br>165 | Trp        | Ala        | Pro        | Leu        | Ser<br>170 | Ser        | Cys        | Pro        | Ser        | Gln<br>175 | Ala        |
| Leu        | Gln        | Leu<br>180 | Ala        | Gly        | Cys        | Leu        | Ser<br>185 | Gln        | Leu        | His        | Ser        | Gly<br>190 | Leu        | Phe        | Leu        |
| Tyr        | Gln        | Gly<br>195 | Leu        | Leu        | Gln        | Ala        | Leu<br>200 | Glu        | Gly        | Ile        | Ser        | Pro<br>205 | Glu        | Leu        | Gly        |
| Pro        | Thr<br>210 | Leu        | Asp        | Thr        | Leu        | Gln<br>215 | Leu        | Asp        | Val        | Ala        | Asp<br>220 | Phe        | Ala        | Thr        | Thr        |
| Ile<br>225 | Trp        | Gln        | Gln        | Met        | Glu<br>230 | Glu        | Leu        | Gly        | Met        | Ala<br>235 | Pro        | Ala        | Leu        | Gln        | Pro<br>240 |
| Thr        | Gln        | Gly        | Ala        | Met<br>245 | Pro        | Ala        | Phe        | Ala        | Ser<br>250 | Ala        | Phe        | Gln        | Arg        | Arg<br>255 | Ala        |
| Gly        | Gly        | Val        | Leu<br>260 | Val        | Ala        | Ser        | His        | Leu<br>265 | Gln        | Ser        | Phe        | Leu        | Glu<br>270 | Val        | Ser        |
| Tyr        | Arg        | Val<br>275 | Leu        | Arg        | His        | Leu        | Ala<br>280 | Gln        | Pro        | Thr        | Pro        | Leu<br>285 | Gly        | Pro        | Ala        |
| Ser        | Ser<br>290 | Leu        | Pro        | Gln        | Ser        | Phe<br>295 | Leu        | Leu        | Lys        | Ser        | Leu<br>300 | Glu        | Gln        | Val        | Arg        |
| Lys<br>305 | Ile        | Gln        | Gly        | Asp        | Gly<br>310 | Ala        | Ala        | Leu        | Gln        | Glu<br>315 | Lys        | Leu        | Cys        | Ala        | Thr<br>320 |

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro  
1 5 10 15

Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser  
 20 25 30  
 Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val  
 35 40 45  
 Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu  
 50 55 60  
 Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg  
 65 70 75 80  
 His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys  
 85 90 95  
 Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Tyr  
 100 105 110  
 Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly Gly Ser  
 115 120 125  
 Asn Met Ala Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp  
 130 135 140  
 Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly  
 145 150 155 160  
 Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala  
 165 170 175  
 Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu  
 180 185 190  
 Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln  
 195 200 205  
 Pro Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu  
 210 215 220  
 Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu  
 225 230 235 240  
 Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu  
 245 250 255  
 Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser  
 260 265 270  
 Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His  
 275 280 285  
 Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile  
 290 295 300  
 Ser  
 305

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Tyr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | Ser |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | Asn |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |
| Met | Ala | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |  |
| Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met |  |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Thr | Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu | Lys |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln |  |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |  |
| Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Met | Ala | Met | Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Ala | Gln | Pro | Thr | Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly  
 195 200 205  
 Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro  
 210 215 220  
 Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro  
 225 230 235 240  
 Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser  
 245 250 255  
 Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu  
 260 265 270  
 Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu  
 275 280 285  
 Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu  
 290 295 300  
 Gly  
 305

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 320 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro  
 1 5 10 15  
 Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser  
 20 25 30  
 Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val  
 35 40 45  
 Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu  
 50 55 60  
 Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg  
 65 70 75 80  
 His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys  
 85 90 95  
 Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Tyr  
 100 105 110





(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Tyr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | Ser |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | Asn |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Met | Ala | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Thr | Pro | Leu | Gly |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr |
| 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu |
|     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Tyr |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asn | Met | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Ala | Gln | Pro | Thr | Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |

Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro  
 210 215 220  
 Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser  
 225 230 235 240  
 Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu  
 245 250 255  
 Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu  
 260 265 270  
 Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu  
 275 280 285  
 Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe  
 290 295 300  
 Ala  
 305

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro  
 1 5 10 15  
 Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser  
 20 25 30  
 Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val  
 35 40 45  
 Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu  
 50 55 60  
 Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg  
 65 70 75 80  
 His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys  
 85 90 95  
 Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Tyr  
 100 105 110  
 Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser  
 115 120 125

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | Asn |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Gln | Pro | Thr | Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Met | Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser | Ile | Leu | Met | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val | Arg | Ala | Val | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu | Arg | Asn | Leu | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg | His | Pro | Ile | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys | Leu | Thr | Phe | Tyr |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Gly | Gly | Gly | Ser | Asn |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro | Pro |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ala | Pro | Leu | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly | Pro | Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Lys | Ser | Pro | Asn | Met | Ala | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ser | Gly | Gly | Ser | Gly | Gly | Ser | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu |  |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |  |
| Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln |  |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Gly | Gly | Gly | Ser | Asn | Cys | Ser | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro | Pro | Ala | Pro | Leu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser | Ile | Leu | Met | Asp |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val | Arg | Ala | Val | Lys |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asn | Leu | Glu | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly | Pro | Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Lys | Ser | Pro | Asn | Met | Ala | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ser | Gly | Gly | Ser | Gly | Gly | Ser | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr |
| 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Arg | Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gln | Gln | Gly | Gly | Gly | Ser | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | His | His | Leu | Lys | Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Asn | Asp | Glu | Asp | Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Asn | Leu | Glu | Ser | Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Gly | Ile | Glu | Ala | Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Thr | Ala | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Pro | Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ser | Pro | Asn | Met | Ala | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Gly | Ser | Gly | Gly | Ser | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Gly | Gly | Gly | Ser | Asn | Cys | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro | Pro | Ala | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser | Ile | Leu | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val | Arg | Ala | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu | Arg | Asn | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg | His | Pro | Ile |

| 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ile | Lys | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Pro | Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ser | Pro | Asn | Met | Ala | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Gly | Gly | Ser | Gly | Gly | Ser | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser | Ile | Leu | Met | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Arg        | Asn        | Leu        | Arg<br>20  | Leu        | Pro        | Asn        | Leu        | Glu<br>25  | Ser        | Phe        | Val        | Arg        | Ala<br>30  | Val        | Lys        |
| Asn        | Leu        | Glu<br>35  | Asn        | Ala        | Ser        | Gly        | Ile<br>40  | Glu        | Ala        | Ile        | Leu        | Arg<br>45  | Asn        | Leu        | Gln        |
| Pro        | Cys<br>50  | Leu        | Pro        | Ser        | Ala        | Thr<br>55  | Ala        | Ala        | Pro        | Ser        | Arg<br>60  | His        | Pro        | Ile        | Ile        |
| Ile<br>65  | Lys        | Ala        | Gly        | Asp        | Trp<br>70  | Gln        | Glu        | Phe        | Arg        | Glu<br>75  | Lys        | Leu        | Thr        | Phe        | Tyr<br>80  |
| Leu        | Val        | Thr        | Leu        | Glu<br>85  | Gln        | Ala        | Gln        | Glu        | Gln<br>90  | Gln        | Gly        | Gly        | Gly        | Ser<br>95  | Gly        |
| Gly        | Gly        | Ser        | Gly<br>100 | Gly        | Gly        | Ser        | Asn        | Cys<br>105 | Ser        | Ile        | Met        | Ile        | Asp<br>110 | Glu        | Ile        |
| Ile        | His        | His<br>115 | Leu        | Lys        | Arg        | Pro        | Pro<br>120 | Ala        | Pro        | Leu        | Tyr        | Val<br>125 | Glu        | Gly        | Gly        |
| Gly        | Gly<br>130 | Ser        | Pro        | Gly        | Glu        | Pro<br>135 | Ser        | Gly        | Pro        | Ile        | Ser<br>140 | Thr        | Ile        | Asn        | Pro        |
| Ser<br>145 | Pro        | Pro        | Ser        | Lys        | Glu<br>150 | Ser        | His        | Lys        | Ser        | Pro<br>155 | Asn        | Met        | Ala        | Thr        | Gln<br>160 |
| Gly        | Ala        | Met        | Pro        | Ala<br>165 | Phe        | Ala        | Ser        | Ala        | Phe<br>170 | Gln        | Arg        | Arg        | Ala        | Gly<br>175 | Gly        |
| Val        | Leu        | Val        | Ala<br>180 | Ser        | His        | Leu        | Gln        | Ser<br>185 | Phe        | Leu        | Glu        | Val        | Ser<br>190 | Tyr        | Arg        |
| Val        | Leu        | Arg<br>195 | His        | Leu        | Ala        | Gln        | Pro<br>200 | Ser        | Gly        | Gly        | Ser        | Gly<br>205 | Gly        | Ser        | Gln        |
| Ser        | Phe<br>210 | Leu        | Leu        | Lys        | Ser        | Leu<br>215 | Glu        | Gln        | Val        | Arg        | Lys<br>220 | Ile        | Gln        | Gly        | Asp        |
| Gly<br>225 | Ala        | Ala        | Leu        | Gln        | Glu<br>230 | Lys        | Leu        | Cys        | Ala        | Thr<br>235 | Tyr        | Lys        | Leu        | Cys        | His<br>240 |
| Pro        | Glu        | Glu        | Leu        | Val<br>245 | Leu        | Leu        | Gly        | His        | Ser<br>250 | Leu        | Gly        | Ile        | Pro        | Trp<br>255 | Ala        |
| Pro        | Leu        | Ser        | Ser<br>260 | Cys        | Pro        | Ser        | Gln        | Ala<br>265 | Leu        | Gln        | Leu        | Ala        | Gly<br>270 | Cys        | Leu        |
| Ser        | Gln        | Leu<br>275 | His        | Ser        | Gly        | Leu        | Phe<br>280 | Leu        | Tyr        | Gln        | Gly        | Leu<br>285 | Leu        | Gln        | Ala        |
| Leu        | Glu<br>290 | Gly        | Ile        | Ser        | Pro        | Glu<br>295 | Leu        | Gly        | Pro        | Thr        | Leu<br>300 | Asp        | Thr        | Leu        | Gln        |
| Leu<br>305 | Asp        | Val        | Ala        | Asp        | Phe<br>310 | Ala        | Thr        | Thr        | Ile        | Trp<br>315 | Gln        | Gln        | Met        | Glu        | Glu<br>320 |
| Leu        | Gly        | Met        | Ala        | Pro<br>325 | Ala        | Leu        | Gln        | Pro        |            |            |            |            |            |            |            |

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Gly | Gly | Ser | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Leu | Lys | Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu | Asp | Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Glu | Ser | Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Tyr | Val | Glu | Gly | Gly |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | Ser | Thr | Ile | Asn | Pro |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | Asn | Met | Ala | Thr | Gln |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Ser | Gly | Gly | Ser | Gly | Gly | Ser | Gln |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 245 |     | 250 |     | 255 |     |     |     |     |     |     |     |     |     |     |
| Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro |     |     |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Arg | Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gln | Gln | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | Pro | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | Ser | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | Val | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | Leu | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Tyr | Val | Glu | Gly | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | Ser | Thr | Ile | Asn | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | Asn | Met | Ala | Thr | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Ser | Gly | Gly | Ser | Gly | Gly | Ser | Gln |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro |     |     |     |     |     |     |     |  |
|     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 299 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Gly | Ser | Gly | Gly | Gly | Ser | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ile | His | His | Leu | Lys | Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Asn | Asp | Glu | Asp | Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro | Asn | Leu | Glu | Ser | Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|
| Ser | Gly | Ile | Glu | Ala | Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | 65  | 70  | 75 | 80  |
| Ala | Thr | Ala | Ala | Pro | Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Tyr | Val | Glu | 85  | 90  |    | 95  |
| Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | Ser | Thr | Ile | 100 | 105 |    | 110 |
| Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | Asn | Met | Ala | 115 | 120 |    | 125 |
| Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | 130 | 135 |    | 140 |
| Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | 145 | 150 |    | 155 |
| Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Ser | Gly | Gly | Ser | Gly | Gly | 165 | 170 |    | 175 |
| Ser | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | 180 | 185 |    | 190 |
| Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | 195 | 200 |    | 205 |
| Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | 210 | 215 |    | 220 |
| Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | 225 | 230 |    | 235 |
| Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | 245 | 250 |    | 255 |
| Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | 260 | 265 |    | 270 |
| Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | 275 | 280 |    | 285 |
| Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro |     |     |     |     |     | 290 | 295 |    |     |

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys

| 1   | 5   | 10  | 15  |
|-----|-----|-----|-----|
| Arg | Pro | Pro | Ala |
| 20  | Pro | Leu | Leu |
| Asp | Pro | Asn | Asn |
| 25  | Leu | Asn | Leu |
| Asp | Pro | Asn | Asp |
| 30  | Glu | Asp |     |
| Val | Ser | Ile | Leu |
| 35  | Met | Asp | Arg |
| 40  | Asn | Leu | Arg |
| 45  | Pro | Asn | Leu |
| Glu | Ser | Gly | Ile |
| 50  | Val | Arg | Ala |
| 55  | Lys | Asn | Leu |
| 60  | Glu | Asn | Ala |
| 65  | Ile | Leu | Arg |
| 70  | Gln | Pro | Cys |
| 75  | Leu | Pro | Ser |
| 80  | Ala | Thr | Ala |
| 85  | Pro | His | Arg |
| 90  | Ile | Ile | Lys |
| 95  | Ala | Gly | Asp |
| 100 | Thr | Leu | Gln |
| 105 | Val | Thr | Leu |
| 110 | Gln | Glu | Gln |
| 115 | Val | Glu | Gly |
| 120 | Gly | Gly | Gly |
| 125 | Gly | Ser | Pro |
| 130 | Ile | Ser | Lys |
| 135 | Thr | Ile | Asn |
| 140 | Pro | Pro | Pro |
| 145 | Pro | Ser | Lys |
| 150 | Glu | Glu | Leu |
| 155 | Val | Leu | Leu |
| 160 | Leu | Leu | Leu |
| 165 | Gly | Ile | Pro |
| 170 | Trp | Ala | Pro |
| 175 | Leu | Ser | Ser |
| 180 | Leu | Gln | Leu |
| 185 | Leu | Gln | Leu |
| 190 | His | Ser | Gly |
| 195 | Tyr | Gln | Gly |
| 200 | Gly | Leu | Leu |
| 205 | Ile | Ser | Pro |
| 210 | Gly | Pro | Thr |
| 215 | Leu | Thr | Leu |
| 220 | Val | Ala | Asp |
| 225 | Met | Ala | Pro |
| 230 | Met | Glu | Gln |
| 235 | Glu | Gln | Gln |
| 240 | Leu | Met | Ala |
| 245 | Ala | Met | Ala |
| 250 | Pro | Met | Ala |
| 255 | Pro | Thr | Gln |
| 260 | Gly | Gly | Val |
| 265 | Leu | Val | Leu |
| 270 | Ser | His | Leu |
| 275 | Pro | Gln | Ser |
| 280 | Ala | Gln | Pro |
| 285 | Gly | Gly | Gly |
| 290 | Met | Ala | Thr |
| 295 | Leu | Gly | Pro |
| 300 | Leu | Pro | Gln |
| 305 | Leu | Lys | Ser |
| 310 | Glu | Gln | Val |
| 315 | Ile | Gln | Gly |
| 320 | Ala | Gly | Asp |
| 325 | Lys | Leu | Cys |
| 330 | Thr | Ala | Cys |
| 335 | Thr | Ala | Cys |
| 340 | Thr | Ala | Cys |
| 345 | Thr | Ala | Cys |
| 350 | Thr | Ala | Cys |
| 355 | Thr | Ala | Cys |
| 360 | Thr | Ala | Cys |
| 365 | Thr | Ala | Cys |
| 370 | Thr | Ala | Cys |
| 375 | Thr | Ala | Cys |
| 380 | Thr | Ala | Cys |
| 385 | Thr | Ala | Cys |
| 390 | Thr | Ala | Cys |
| 395 | Thr | Ala | Cys |
| 400 | Thr | Ala | Cys |
| 405 | Thr | Ala | Cys |
| 410 | Thr | Ala | Cys |
| 415 | Thr | Ala | Cys |
| 420 | Thr | Ala | Cys |
| 425 | Thr | Ala | Cys |
| 430 | Thr | Ala | Cys |
| 435 | Thr | Ala | Cys |
| 440 | Thr | Ala | Cys |
| 445 | Thr | Ala | Cys |
| 450 | Thr | Ala | Cys |
| 455 | Thr | Ala | Cys |
| 460 | Thr | Ala | Cys |
| 465 | Thr | Ala | Cys |
| 470 | Thr | Ala | Cys |
| 475 | Thr | Ala | Cys |
| 480 | Thr | Ala | Cys |
| 485 | Thr | Ala | Cys |
| 490 | Thr | Ala | Cys |
| 495 | Thr | Ala | Cys |
| 500 | Thr | Ala | Cys |

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Asn | Met | Ala | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gln | Pro | Gly | Gly | Gly | Ser | Asp | Met | Ala | Thr | Pro | Leu | Gly | Pro | Ala | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys  
 245 250 255  
 Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr  
 260 265 270  
 Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly  
 275 280 285  
 Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu  
 290 295 300  
 Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly  
 305 310 315 320  
 Leu Leu Gln Ala Leu Glu Gly Ile Ser  
 325

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 329 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
 20 25 30  
 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
 35 40 45  
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro  
 115 120 125  
 Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser  
 130 135 140  
 Pro Asn Met Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     | 150 |     | 155 |     | 160 |     |     |     |     |     |     |     |     |     |
| Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Leu | Ala | Gln | Pro | Gly | Gly | Gly | Ser | Asp | Met | Ala | Thr | Pro | Leu | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala |     |     |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 329 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | 65  | 70  | 75  | 80  |
| Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | 85  | 90  | 95  |     |
| Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | 100 | 105 | 110 |     |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | 115 | 120 | 125 |     |
| Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | 130 | 135 | 140 |     |
| Pro | Asn | Met | Ala | Met | Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | 145 | 150 | 155 | 160 |
| Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | 165 | 170 | 175 |     |
| Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | 180 | 185 | 190 |     |
| His | Leu | Ala | Gln | Pro | Gly | Gly | Gly | Ser | Asp | Met | Ala | Thr | Pro | Leu | Gly | 195 | 200 | 205 |     |
| Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | 210 | 215 | 220 |     |
| Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | 225 | 230 | 235 | 240 |
| Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | 245 | 250 | 255 |     |
| Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | 260 | 265 | 270 |     |
| Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | 275 | 280 | 285 |     |
| Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly | 290 | 295 | 300 |     |
| Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr | 305 | 310 | 315 | 320 |
| Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly |     |     |     |     |     |     |     | 325 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Asn | Met | Ala | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Gly | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Ser | Asp | Met | Ala | Thr | Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln |

|                                                                 |  |     |  |     |
|-----------------------------------------------------------------|--|-----|--|-----|
| 290                                                             |  | 295 |  | 300 |
| Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu |  |     |  |     |
| 305                                                             |  | 310 |  | 315 |
|                                                                 |  |     |  | 320 |
| Leu Gly Met Ala Pro Ala Leu Gln Pro                             |  |     |  |     |
|                                                                 |  | 325 |  |     |

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys |     |     |     |     |
| 1                                                               | 5   | 10  | 15  |     |
| Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp |     |     |     |     |
|                                                                 | 20  | 25  | 30  |     |
| Gln Asp Ile Leu Met Asp Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala |     |     |     |     |
|                                                                 | 35  | 40  | 45  |     |
| Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser |     |     |     |     |
|                                                                 | 50  | 55  | 60  |     |
| Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro |     |     |     |     |
|                                                                 | 65  | 70  | 75  | 80  |
| Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg |     |     |     |     |
|                                                                 | 85  | 90  | 95  |     |
| Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln |     |     |     |     |
|                                                                 | 100 | 105 | 110 |     |
| Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro |     |     |     |     |
|                                                                 | 115 | 120 | 125 |     |
| Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser |     |     |     |     |
|                                                                 | 130 | 135 | 140 |     |
| Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe |     |     |     |     |
|                                                                 | 145 | 150 | 155 | 160 |
| Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe |     |     |     |     |
|                                                                 | 165 | 170 | 175 |     |
| Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly |     |     |     |     |
|                                                                 | 180 | 185 | 190 |     |
| Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val |     |     |     |     |
|                                                                 | 195 | 200 | 205 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly | Pro |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 322 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Cys | Ser | Asn | Met | Ile | Asp | Glu | Ile | Ile | Thr | His | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Pro | Pro | Leu | Pro | Leu | Leu | Asp | Phe | Asn | Asn | Leu | Asn | Gly | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Asp | Ile | Leu | Met | Glu | Asn | Asn | Leu | Arg | Arg | Pro | Asn | Leu | Glu | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Asn | Arg | Ala | Val | Lys | Ser | Leu | Gln | Asn | Ala | Ser | Ala | Ile | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Lys | Asn | Leu | Leu | Pro | Cys | Leu | Pro | Leu | Ala | Thr | Ala | Ala | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Arg | His | Pro | Ile | Ile | Ile | Arg | Asp | Gly | Asp | Trp | Asn | Glu | Phe | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Lys | Leu | Thr | Phe | Tyr | Leu | Lys | Thr | Leu | Glu | Asn | Ala | Gln | Ala | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |



| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Asn | Arg | Ala | Val | Lys | Ser | Leu | Gln | Asn | Ala | Ser | Ala | Ile | Glu | Ser |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Lys | Asn | Leu | Leu | Pro | Cys | Leu | Pro | Leu | Ala | Thr | Ala | Ala | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Arg | His | Pro | Ile | Ile | Ile | Arg | Asp | Gly | Asp | Trp | Asn | Glu | Phe | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Lys | Leu | Thr | Phe | Tyr | Leu | Lys | Thr | Leu | Glu | Asn | Ala | Gln | Ala | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     | Pro |
| Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Asn | Met | Ala | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe |
| 145 |     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Ser | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Ser | Gly | Gly | Ser | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | Ser |
| 225 |     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly | Pro |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro |     |
| 305 |     |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 322 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Asn | Cys | Ser | Asn | Met | Ile | Asp | Glu | Ile | Ile | Thr | His | Leu | Lys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gln | Pro | Pro | Leu | Pro | Leu | Leu | Asp | Phe | Asn | Asn | Leu | Asn | Gly | Glu | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gln | Asp | Ile | Leu | Met | Asp | Asn | Asn | Leu | Arg | Arg | Pro | Asn | Leu | Glu | Ala |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Phe | Asn | Arg | Ala | Val | Lys | Ser | Leu | Gln | Asn | Ala | Ser | Ala | Ile | Glu | Ser |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Leu | Lys | Asn | Leu | Leu | Pro | Cys | Leu | Pro | Leu | Ala | Thr | Ala | Ala | Pro |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Thr | Arg | His | Pro | Ile | His | Ile | Lys | Asp | Gly | Asp | Trp | Asn | Glu | Phe | Arg |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Arg | Lys | Leu | Thr | Phe | Tyr | Leu | Lys | Thr | Leu | Glu | Asn | Ala | Gln | Ala | Gln |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Pro | Asn | Met | Ala | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Thr | Pro |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu |  |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |  |
| Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |

Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala  
 290 295 300  
 Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu  
 305 310 315 320  
 Gln Pro

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg  
 1 5 10 15  
 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val  
 20 25 30  
 Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe  
 35 40 45  
 Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile  
 50 55 60  
 Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser  
 65 70 75 80  
 Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu  
 85 90 95  
 Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
 100 105 110  
 Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile  
 115 120 125  
 Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
 130 135 140  
 Asn Met Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val  
 145 150 155 160  
 Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala  
 165 170 175  
 Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala  
 180 185 190  
 Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Leu | Met | Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Cys | Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

|           |           |            |            |           |           |           |            |            |           |           |           |            |            |           |           |
|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|
| Ala<br>1  | Asn       | Cys        | Ser        | Ile<br>5  | Met       | Ile       | Asp        | Glu        | Ile<br>10 | Ile       | His       | His        | Leu        | Lys<br>15 | Arg       |
| Pro       | Pro       | Ala        | Pro<br>20  | Leu       | Leu       | Asp       | Pro        | Asn<br>25  | Asn       | Leu       | Asn       | Asp        | Glu<br>30  | Asp       | Val       |
| Ser       | Ile       | Leu<br>35  | Met        | Asp       | Arg       | Asn       | Leu<br>40  | Arg        | Leu       | Pro       | Asn       | Leu<br>45  | Glu        | Ser       | Phe       |
| Val       | Arg<br>50 | Ala        | Val        | Lys       | Asn       | Leu<br>55 | Glu        | Asn        | Ala       | Ser       | Gly<br>60 | Ile        | Glu        | Ala       | Ile       |
| Leu<br>65 | Arg       | Asn        | Leu        | Gln       | Pro<br>70 | Cys       | Leu        | Pro        | Ser       | Ala<br>75 | Thr       | Ala        | Ala        | Pro       | Ser<br>80 |
| Arg       | His       | Pro        | Ile        | Ile<br>85 | Ile       | Lys       | Ala        | Gly        | Asp<br>90 | Trp       | Gln       | Glu        | Phe        | Arg<br>95 | Glu       |
| Lys       | Leu       | Thr        | Phe<br>100 | Tyr       | Leu       | Val       | Thr        | Leu<br>105 | Glu       | Gln       | Ala       | Gln        | Glu<br>110 | Gln       | Gln       |
| Tyr       | Val       | Glu<br>115 | Gly        | Gly       | Gly       | Gly       | Ser<br>120 | Pro        | Gly       | Glu       | Pro       | Ser<br>125 | Gly        | Pro       | Ile       |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Met | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Gly | Asn | Met | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| His | Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | 50  | 55  | 60  |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | 65  | 70  | 75  | 80  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | 85  | 90  | 95  |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | 100 | 105 | 110 |     |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | 115 | 120 | 125 |     |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | 130 | 135 | 140 |     |
| Asn | Met | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | 145 | 150 | 155 | 160 |
| Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | 165 | 170 | 175 |     |
| Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | 180 | 185 | 190 |     |
| Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | 195 | 200 | 205 |     |
| Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | 210 | 215 | 220 |     |
| Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln | 225 | 230 | 235 | 240 |
| His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu | Val | Gly | Gly | Ser | 245 | 250 | 255 |     |
| Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Gly | Asn | Met | Ala | Ser | Pro | Ala | Pro | 260 | 265 | 270 |     |
| Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | 275 | 280 | 285 |     |
| Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | 290 | 295 | 300 |     |
| Thr | Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 305 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Asn | Met | Ala | Val | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Gly | Val | Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| His | Lys | Asp | Pro | Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Gly | Lys | Val | Arg | Phe | Leu | Met | Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Arg | Glu | Phe | Gly | Gly | Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |

Leu Pro  
305

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 306 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Met | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Leu | Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Pro | Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | 225 | 230 | 235 | 240 |
| Val | Arg | Phe | Leu | Met | Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | 245 | 250 | 255 |     |
| Phe | Gly | Gly | Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | 260 | 265 | 270 |     |
| Val | Leu | Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | 275 | 280 | 285 |     |
| Ser | Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | 290 | 295 | 300 |     |
| Ala | Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 305 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | 1   | 5   | 10  | 15 |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | 20  | 25  | 30  |    |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | 35  | 40  | 45  |    |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | 50  | 55  | 60  |    |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | 65  | 70  | 75  | 80 |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | 85  | 90  | 95  |    |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | 100 | 105 | 110 |    |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | 115 | 120 | 125 |    |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | 130 | 135 | 140 |    |
| Asn | Met | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp |     |     |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     | 150 |     | 155 |     | 160 |     |     |     |     |     |     |     |     |     |
| Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Met | Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Gly | Asn |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Asn | Met | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Gly | Asn | Met |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile |  |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |  |
| Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly |  |
|     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |  |
| Gln | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |  |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Asn | Met | Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Asp | Pro | Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Val | Arg | Phe | Leu | Met | Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Phe | Gly | Gly | Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Val | Leu | Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Ser | Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Ala | Val | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| Gly | Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Leu | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | 1   | 5   | 10  | 15  |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | 20  | 25  | 30  |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | 35  | 40  | 45  |     |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | 50  | 55  | 60  |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | 65  | 70  | 75  | 80  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | 85  | 90  | 95  |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | 100 | 105 | 110 |     |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | 115 | 120 | 125 |     |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | 130 | 135 | 140 |     |
| Asn | Met | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe | Leu | 145 | 150 | 155 | 160 |
| Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu | Val | 165 | 170 | 175 |     |
| Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Gly | Asn | Met | Ala | Ser | 180 | 185 | 190 |     |
| Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu | Arg | 195 | 200 | 205 |     |
| Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | His | 210 | 215 | 220 |     |
| Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu | Gly | 225 | 230 | 235 | 240 |
| Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly | 245 | 250 | 255 |     |

Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu  
260 265 270

Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val  
275 280 285

Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro  
290 295 300

Pro Gln  
305

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg  
1 5 10 15

Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val  
20 25 30

Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe  
35 40 45

Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile  
50 55 60

Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser  
65 70 75 80

Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu  
85 90 95

Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
100 105 110

Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile  
115 120 125

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
130 135 140

Asn Met Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His  
145 150 155 160

Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr  
165 170 175

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Leu | Cys | Val | Arg | Glu | Phe | Gly | Gly | Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Thr | Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |  |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |  |  |

| 100 |     |     |     |     |     |     |     |     |     | 105 |     |     |     |     | 110 |  |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |  |  |  |  |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |  |  |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |  |  |  |  |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |  |  |  |
| Asn | Met | Asp | Pro | Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg |  |  |  |  |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |  |  |
| Gly | Lys | Val | Arg | Phe | Leu | Met | Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val |  |  |  |  |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |  |  |  |  |
| Arg | Glu | Phe | Gly | Gly | Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp |  |  |  |  |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |  |  |  |  |
| Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser |  |  |  |  |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |  |  |
| Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu |  |  |  |  |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |  |  |  |
| Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu |  |  |  |  |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |  |  |  |  |
| Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu |  |  |  |  |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |  |  |  |  |
| Gly | Val | Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser |  |  |  |  |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |  |  |  |  |
| Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu |  |  |  |  |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |  |  |  |
| Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala |  |  |  |  |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |  |  |
| His | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 306 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe  
 35 40 45  
 Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile  
 50 55 60  
 Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser  
 65 70 75 80  
 Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu  
 85 90 95  
 Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
 100 105 110  
 Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile  
 115 120 125  
 Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
 130 135 140  
 Asn Met Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val  
 145 150 155 160  
 Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe  
 165 170 175  
 Gly Gly Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val  
 180 185 190  
 Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser  
 195 200 205  
 Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala  
 210 215 220  
 Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys  
 225 230 235 240  
 Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met  
 245 250 255  
 Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly  
 260 265 270  
 Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu  
 275 280 285  
 Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp  
 290 295 300  
 Pro Asn  
 305

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Asn | Met | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Phe | Leu | Met | Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser |  |

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
|     | 275 |     | 280 |     | 285 |     |
| Lys | Leu | Leu | Arg | Asp | Ser | His |
|     | 290 |     |     |     |     | 295 |
|     |     |     |     |     |     |     |
| Val | Leu | His | Ser | Arg | Leu | Ser |
|     |     |     |     | 300 |     |     |
| Gln | Cys |     |     |     |     |     |
|     |     |     |     |     |     |     |
| Pro |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Met | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu |
| 210 |     |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Asn | Met | Ala | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu | Arg |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | His |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
 130 135 140  
 Asn Met Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys  
 145 150 155 160  
 Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr  
 165 170 175  
 Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr  
 180 185 190  
 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu  
 195 200 205  
 Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly  
 210 215 220  
 Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln  
 225 230 235 240  
 His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser  
 245 250 255  
 Thr Leu Cys Val Arg Glu Phe Gly Asn Met Ala Ser Pro Ala Pro Pro  
 260 265 270  
 Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val  
 275 280 285  
 Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr  
 290 295 300  
 Pro  
 305

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg  
 1 5 10 15  
 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val  
 20 25 30  
 Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe  
 35 40 45  
 Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile

| 50                                                              | 55  | 60          |
|-----------------------------------------------------------------|-----|-------------|
| Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser |     |             |
| 65                                                              | 70  | 75 80       |
| Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu |     |             |
|                                                                 | 85  | 90 95       |
| Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln |     |             |
|                                                                 | 100 | 105 110     |
| Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile |     |             |
|                                                                 | 115 | 120 125     |
| Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro |     |             |
|                                                                 | 130 | 135 140     |
| Asn Met Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu |     |             |
|                                                                 | 145 | 150 155 160 |
| Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu |     |             |
|                                                                 | 165 | 170 175     |
| Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser |     |             |
|                                                                 | 180 | 185 190     |
| Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu |     |             |
|                                                                 | 195 | 200 205     |
| Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala |     |             |
|                                                                 | 210 | 215 220     |
| His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg |     |             |
|                                                                 | 225 | 230 235 240 |
| Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val |     |             |
|                                                                 | 245 | 250 255     |
| Arg Glu Phe Gly Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu |     |             |
|                                                                 | 260 | 265 270     |
| Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg |     |             |
|                                                                 | 275 | 280 285     |
| Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu |     |             |
|                                                                 | 290 | 295 300     |
| Pro                                                             |     |             |
| 305                                                             |     |             |

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |
| Asn | Met | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Gly | Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Leu | Leu | Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Asp | Pro | Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Val | Arg | Phe | Leu | Met | Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Phe | Gly | Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Leu | Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |

Val  
305

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 305 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: unknown  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |
| Asn | Met | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |  |
| Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |  |
| Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 225 |     | 230 |     | 235 |     | 240 |     |     |     |     |     |     |     |     |     |
| Met | Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Asn | Met |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Met | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln  
 165 170 175  
 Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile  
 180 185 190  
 Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met  
 195 200 205  
 Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe Gly Asn Met Ala  
 210 215 220  
 Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu  
 225 230 235 240  
 Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val  
 245 250 255  
 His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu  
 260 265 270  
 Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu  
 275 280 285  
 Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln  
 290 295 300  
 Leu  
 305

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg  
 1 5 10 15  
 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val  
 20 25 30  
 Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe  
 35 40 45  
 Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile  
 50 55 60  
 Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser  
 65 70 75 80

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |     |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Asn | Met | Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Asp | Pro | Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Val | Arg | Phe | Leu | Met | Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Phe | Gly | Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Leu | Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Val | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg

| 1                                                               | 5   | 10  | 15  |
|-----------------------------------------------------------------|-----|-----|-----|
| Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val | 20  | 25  | 30  |
| Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe | 35  | 40  | 45  |
| Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile | 50  | 55  | 60  |
| Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser | 65  | 70  | 75  |
| Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu | 85  | 90  | 95  |
| Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln | 100 | 105 | 110 |
| Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile | 115 | 120 | 125 |
| Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro | 130 | 135 | 140 |
| Asn Met Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu | 145 | 150 | 155 |
| Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val | 165 | 170 | 175 |
| Gly Gly Ser Thr Leu Cys Val Arg Glu Phe Gly Asn Met Ala Ser Pro | 180 | 185 | 190 |
| Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp | 195 | 200 | 205 |
| Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro | 210 | 215 | 220 |
| Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu | 225 | 230 | 235 |
| Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala | 245 | 250 | 255 |
| Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly | 260 | 265 | 270 |
| Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg | 275 | 280 | 285 |
| Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro | 290 | 295 | 300 |
| Gln                                                             |     |     |     |
| 305                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 305 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | 1   | 5   | 10  | 15  |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | 20  | 25  | 30  |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | 35  | 40  | 45  |     |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | 50  | 55  | 60  |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | 65  | 70  | 75  | 80  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | 85  | 90  | 95  |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | 100 | 105 | 110 |     |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | 115 | 120 | 125 |     |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | 130 | 135 | 140 |     |
| Asn | Met | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe | Leu | 145 | 150 | 155 | 160 |
| Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu | Val | 165 | 170 | 175 |     |
| Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Asn | Met | Ala | Ser | Pro | 180 | 185 | 190 |     |
| Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu | Arg | Asp | 195 | 200 | 205 |     |
| Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | His | Pro | 210 | 215 | 220 |     |
| Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu | Gly | Glu | 225 | 230 | 235 | 240 |
| Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | 245 | 250 | 255 |     |

Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly  
260 265 270

Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg  
275 280 285

Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro  
290 295 300

Gln  
305

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 305 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg  
1 5 10 15

Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val  
20 25 30

Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe  
35 40 45

Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile  
50 55 60

Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser  
65 70 75 80

Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu  
85 90 95

Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
100 105 110

Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile  
115 120 125

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
130 135 140

Asn Met Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg  
145 150 155 160

Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val  
165 170 175

Arg Glu Phe Gly Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 180 |     | 185 |     | 190 |     |     |     |     |     |     |     |     |     |     |
| Arg | Val | Leu | Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Ser | Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Pro | Ala | Val | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Gly | Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ser | Leu | Leu | Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 305 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile  
 115 120 125  
 Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
 130 135 140  
 Asn Met Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val  
 145 150 155 160  
 Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe  
 165 170 175  
 Gly Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu  
 180 185 190  
 Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln  
 195 200 205  
 Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val  
 210 215 220  
 Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala  
 225 230 235 240  
 Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala  
 245 250 255  
 Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln  
 260 265 270  
 Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu  
 275 280 285  
 Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro  
 290 295 300  
 Asn  
 305

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg  
 1 5 10 15  
 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val  
 20 25 30

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | 35  | 40  | 45  |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | 50  | 55  | 60  |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | 65  | 70  | 75  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | 85  | 90  | 95  |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | 100 | 105 | 110 |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | 115 | 120 | 125 |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | 130 | 135 | 140 |
| Asn | Met | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu | 145 | 150 | 155 |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | 165 | 170 | 175 |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln | 180 | 185 | 190 |
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln | 195 | 200 | 205 |
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu | 210 | 215 | 220 |
| Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe | 225 | 230 | 235 |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu | 245 | 250 | 255 |
| Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Gly | Asn | Gly | Gly | 260 | 265 | 270 |
| Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | 275 | 280 | 285 |
| Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | 290 | 295 | 300 |
| Pro | Glu | Val | His | Pro |     |     |     |     |     |     |     |     |     |     |     | 305 |     |     |

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |  |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Asn | Met | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu |  |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |  |  |
| Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu |  |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Gly | Asn | Gly | Gly |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |

Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys  
 290 295 300

Pro Glu Val His Pro  
 305

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | 1   | 5   | 10  | 15  |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | 20  | 25  | 30  |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | 35  | 40  | 45  |     |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | 50  | 55  | 60  |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | 65  | 70  | 75  | 80  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | 85  | 90  | 95  |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | 100 | 105 | 110 |     |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | 115 | 120 | 125 |     |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | 130 | 135 | 140 |     |
| Asn | Met | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | 145 | 150 | 155 | 160 |
| Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | 165 | 170 | 175 |     |
| Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | 180 | 185 | 190 |     |
| Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | 195 | 200 | 205 |     |

Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly  
 210 215 220  
 Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln  
 225 230 235 240  
 His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser  
 245 250 255  
 Thr Leu Cys Val Arg Glu Phe Gly Gly Asn Gly Gly Asn Met Ala Ser  
 260 265 270  
 Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg  
 275 280 285  
 Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His  
 290 295 300  
 Pro Leu Pro Thr Pro  
 305

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg  
 1 5 10 15  
 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val  
 20 25 30  
 Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe  
 35 40 45  
 Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile  
 50 55 60  
 Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser  
 65 70 75 80  
 Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu  
 85 90 95  
 Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
 100 105 110  
 Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile  
 115 120 125  
 Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| 130                                                             |     | 135 |     | 140 |
| Asn Met Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu |     |     |     |     |
| 145                                                             |     | 150 |     | 155 |
| Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu |     |     |     |     |
|                                                                 | 165 |     | 170 | 175 |
| Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser |     |     |     |     |
|                                                                 | 180 |     | 185 | 190 |
| Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu |     |     |     |     |
|                                                                 | 195 |     | 200 | 205 |
| Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala |     |     |     |     |
|                                                                 | 210 |     | 215 | 220 |
| His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg |     |     |     |     |
| 225                                                             |     | 230 |     | 235 |
| Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val |     |     |     |     |
|                                                                 | 245 |     | 250 | 255 |
| Arg Glu Phe Gly Gly Asn Gly Gly Asn Met Ala Ser Pro Ala Pro Pro |     |     |     |     |
|                                                                 | 260 |     | 265 | 270 |
| Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val |     |     |     |     |
|                                                                 | 275 |     | 280 | 285 |
| Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr |     |     |     |     |
|                                                                 | 290 |     | 295 | 300 |
| Pro Val Leu Leu Pro                                             |     |     |     |     |
| 305                                                             |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

|                                                                 |
|-----------------------------------------------------------------|
| Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg |
| 1 5 10 15                                                       |
| Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val |
| 20 25 30                                                        |
| Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe |
| 35 40 45                                                        |
| Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile |
| 50 55 60                                                        |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | 65  | 70  | 75  | 80  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | 85  | 90  | 95  |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | 100 | 105 | 110 |     |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | 115 | 120 | 125 |     |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | 130 | 135 | 140 |     |
| Asn | Met | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | 145 | 150 | 155 | 160 |
| Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | 165 | 170 | 175 |     |
| Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | 180 | 185 | 190 |     |
| Gly | Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | 195 | 200 | 205 |     |
| Leu | Leu | Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | 210 | 215 | 220 |     |
| Asp | Pro | Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | 225 | 230 | 235 | 240 |
| Val | Arg | Phe | Leu | Met | Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | 245 | 250 | 255 |     |
| Phe | Gly | Gly | Asn | Gly | Gly | Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | 260 | 265 | 270 |     |
| Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | 275 | 280 | 285 |     |
| Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | 290 | 295 | 300 |     |
| Leu | Leu | Pro | Ala | Val |     |     |     |     |     |     |     |     |     |     |     | 305 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

[illegible]

## (2) INFORMATION FOR SEQ ID NO:233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | 1   | 5   | 10  | 15  |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | 20  | 25  | 30  |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | 35  | 40  | 45  |     |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | 50  | 55  | 60  |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | 65  | 70  | 75  | 80  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | 85  | 90  | 95  |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | 100 | 105 | 110 |     |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | 115 | 120 | 125 |     |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | 130 | 135 | 140 |     |
| Asn | Met | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | 145 | 150 | 155 | 160 |
| Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | 165 | 170 | 175 |     |
| Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | 180 | 185 | 190 |     |
| Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | 195 | 200 | 205 |     |
| Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg | Glu | Phe | Gly | Gly | Asn | Gly | 210 | 215 | 220 |     |
| Gly | Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | 225 | 230 | 235 | 240 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Arg | Gly | Gln | Leu |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Met | Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys  
 165 170 175  
 Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu  
 180 185 190  
 Phe Gly Gly Asn Gly Gly Asn Met Ala Ser Pro Ala Pro Pro Ala Cys  
 195 200 205  
 Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His  
 210 215 220  
 Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val  
 225 230 235 240  
 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met  
 245 250 255  
 Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu  
 260 265 270  
 Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser  
 275 280 285  
 Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala  
 290 295 300  
 Leu Gln Ser Leu Leu  
 305

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg  
 1 5 10 15  
 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val  
 20 25 30  
 Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe  
 35 40 45  
 Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile  
 50 55 60  
 Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser  
 65 70 75 80  
 Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu



Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val  
 20 25 30  
 Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe  
 35 40 45  
 Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile  
 50 55 60  
 Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser  
 65 70 75 80  
 Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu  
 85 90 95  
 Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
 100 105 110  
 Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile  
 115 120 125  
 Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
 130 135 140  
 Asn Met Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His  
 145 150 155 160  
 Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr  
 165 170 175  
 Leu Cys Val Arg Glu Phe Gly Gly Asn Gly Gly Asn Met Ala Ser Pro  
 180 185 190  
 Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp  
 195 200 205  
 Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro  
 210 215 220  
 Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu  
 225 230 235 240  
 Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala  
 245 250 255  
 Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly  
 260 265 270  
 Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg  
 275 280 285  
 Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro  
 290 295 300  
 Gln Gly Arg Thr Thr  
 305

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg | 1   | 5   | 10  | 15  |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val | 20  | 25  | 30  |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe | 35  | 40  | 45  |     |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile | 50  | 55  | 60  |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser | 65  | 70  | 75  | 80  |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu | 85  | 90  | 95  |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln | 100 | 105 | 110 |     |
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | 115 | 120 | 125 |     |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | 130 | 135 | 140 |     |
| Asn | Met | Asp | Pro | Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | 145 | 150 | 155 | 160 |
| Gly | Lys | Val | Arg | Phe | Leu | Met | Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | 165 | 170 | 175 |     |
| Arg | Glu | Phe | Gly | Gly | Asn | Gly | Gly | Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | 180 | 185 | 190 |     |
| Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val | 195 | 200 | 205 |     |
| Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr | 210 | 215 | 220 |     |
| Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | 225 | 230 | 235 | 240 |
| Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | 245 | 250 | 255 |     |
| Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys |     |     |     |     |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 260                                                             | 265 | 270 |
| Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu |     |     |
| 275                                                             | 280 | 285 |
| Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg |     |     |
| 290                                                             | 295 | 300 |
| Thr Thr Ala His Lys                                             |     |     |
| 305                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg |     |     |
| 1                                                               | 5   | 10  |
| Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val |     |     |
| 20                                                              | 25  | 30  |
| Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe |     |     |
| 35                                                              | 40  | 45  |
| Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile |     |     |
| 50                                                              | 55  | 60  |
| Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser |     |     |
| 65                                                              | 70  | 75  |
| Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu |     |     |
| 85                                                              | 90  | 95  |
| Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln |     |     |
| 100                                                             | 105 | 110 |
| Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile |     |     |
| 115                                                             | 120 | 125 |
| Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro |     |     |
| 130                                                             | 135 | 140 |
| Asn Met Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val |     |     |
| 145                                                             | 150 | 155 |
| Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe |     |     |
| 165                                                             | 170 | 175 |
| Gly Gly Asn Gly Gly Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp |     |     |
| 180                                                             | 185 | 190 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Val | Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| His | Lys | Asp | Pro | Asn |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 302 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | Ile |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | Ile | 115 | 120 | 125 |
| Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | Pro | 130 | 135 | 140 |
| Asn | Met | Asp | Pro | Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | 145 | 150 | 155 |
| Gly | Lys | Val | Arg | Phe | Leu | Met | Leu | Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | 165 | 170 | 175 |
| Arg | Glu | Phe | Gly | Gly | Asn | Met | Ala | Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | 180 | 185 | 190 |
| Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | 195 | 200 | 205 |
| Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu | 210 | 215 | 220 |
| Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | 225 | 230 | 235 |
| Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | 245 | 250 | 255 |
| Gly | Val | Met | Ala | Ala | Arg | Gly | Gln | Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | 260 | 265 | 270 |
| Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | 275 | 280 | 285 |
| Gln | Ser | Leu | Leu | Gly | Thr | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys |     |     | 290 | 295 | 300 |

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

AATTCGTCG TAAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT  
60

ACGTAGAGGG CGGTGGAGGC TCC  
83

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

CCGGGGAGCC TCCACGCCCC TCTACGTACT GTTGAGCCTG CGCGTTCTCC AAGGTTTTCA  
60

GATAGAAGGT CAGTTTACGA CGG  
83

- (2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Gly Gly Gly Ser Gly Gly Gly Ser  
1 5

- (2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
1 5 10

- (2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Ser Gly Gly Ser Gly Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Glu Phe Gly Asn Met Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Glu Phe Gly Gly Asn Met Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Glu Phe Gly Gly Asn Gly Gly Asn Met Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Gly Gly Ser Asp Met Ala Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 459 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGA CTCCCAT  
60

GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACC CTTTGCCTAC ACCTGTCCTG  
120

CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA  
180

CAGGACATTC TGGGAGCAGT GACCCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA  
240

CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC  
300

CTTGGGGCCC TGCAGAGCCT CCTTGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT  
360

CACAAGGATC CCAATGCCAT TTCTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT  
420

TTCTTGATGC TTGTAGGAGG GTCCACCCTC TCGTCAGG

459

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

TCTCCCGCTC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGA TCTCCCAT  
60

GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTCAAC CTTTGCCTAC ACCTGTCCTG  
120

CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA  
180

CAGGACATTC TGGGAGCAGT GACCCCTTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA  
240

CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC  
300

CTTGGGGCCC TGCAGAGCCT CCTTGGAACC CAGGGCAGGA CCACAGCTCA CAAGGATCCC  
360

AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT CCTGATGCTT  
420

GTAGGAGGGT CCACCCCTCTG CGTCAGG  
447

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TCCCCAGCGC CGCCTGCTTG TGACCTCCGA GTCCTCAGTA AACTGCTTCG TGA TCTCCCAT  
60

GTCCTTCACA GCAGACTGAG CCAGTGCCCA GAGGTTACC CTTGCCTAC ACCTGTCCTG  
120

CTGCCTGCTG TGGACTTTAG CTTGGGAGAA TGGAAAACCC AGATGGAGGA GACCAAGGCA  
180

CAGGACATTC TGGGAGCAGT GACCCCTCTG CTGGAGGGAG TGATGGCAGC ACGGGGACAA  
240

CTGGGACCCA CTTGCCTCTC ATCCCTCCTG GGGCAGCTTT CTGGACAGGT CCGTCTCCTC  
300

CTTGGGGCCC TGCAGAGCCT CCTTGAACC CAGCTTCCTC CACAGGGCAG GACCACAGCT  
360

CACAAGGATC CCAATGCCAT CTTCTGAGC TTCCAACACC TGCTCCGAGG AAAGGTGCGT  
420

TTCCTGATGC TTGTAGGAGG GTCCACCCTC TCGTCAGG  
459

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu |

|                                     |     |     |
|-------------------------------------|-----|-----|
| 130                                 | 135 | 140 |
| Val Gly Gly Ser Thr Leu Cys Val Arg |     |     |
| 145                                 | 150 |     |

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 149 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe | Leu | Ser | Phe | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu | Val | Gly | Gly | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Leu | Cys | Val | Arg |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Pro | Ala | Pro | Pro | Ala | Cys | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Leu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Val | Gly | Gly | Ser | Thr | Leu | Cys | Val | Arg |     |     |     |     |     |     |     |  |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GGATCCACCA TGAGCCGCCT GCCCGTCCTG CTCCTGCTCC AACTCCTGGT CCGCCCCGCC  
60

ATGG  
64

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 112

(D) OTHER INFORMATION: /note= "position 112 is deleted or  
Leu, Ala, Val, Ile, Pro, Phe, Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 113

(D) OTHER INFORMATION: /note= "positoin 113 is deleted or  
Pro, Phe, Ala, Val, Leu, Ile, Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 114

(D) OTHER INFORMATION: /note= "position 114 is deleted or  
Pro, Phe, Ala, Val, Leu, Ile, Trp or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 115

(D) OTHER INFORMATION: /note= "positon 115 is deleted or  
Gln, Gly, Ser, Thr, Tyr, or Asn"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu  
1 5 10 15

Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val  
20 25 30

His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu  
35 40 45

Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu  
50 55 60

Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln  
65 70 75 80

Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln  
85 90 95

Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Xaa  
100 105 110

Xaa Xaa Xaa Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe  
115 120 125

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu  
130 135 140

Val Gly Gly Ser Thr Leu Cys Val Arg

145

150

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

CCATGGCTAA CTGCTCTATA ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTG  
60

CACCTTTGCT GGACCCGAAC AACCTCAATG ACGAAGACGT CTCTATCCTG ATGGATCGAA  
120

ACCTTCGACT TCCAAACCTG GAGAGCTTCG TAAGGGCTGT CAAGAACTTA GAAAATGCAT  
180

CAGGTATTGA GGCAATTCTT CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC  
240

CCTCTCGACA TCCAATCATC ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAACTGA  
300

CGTTCTATCT GGTACCCTT GAGCAAGCGC AGGAACAACA GTACGTAGAG GGCGGTGGAG  
360

GCTCCCCGGG TGAACCGTCT GGTCCAATCT CTACTATCAA CCCGTCTCCT CCGTCTAAAG  
420

AATCTCATAA ATCTCCAAAC ATGTAAGGTA CCGCATGCAA GCTT  
464

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "SYNTHETIC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

AAAACAAGAA GAAAGGCGAT AAAAAGGTTG TGGTAAGAGA AATGGATAAA AAGGGGTCGG  
60

GGAAGGAAGG TGGGAGTTAA AAAAGAGGAA GTAGGTCAAG  
100

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

ACGTACTCCA TGGCTAACTG CTCTATAATG ATCGATGAAA TTATACATCA CTTAAAGAGA  
60

CCACCTGCAC CTTTGCTGGA CCCGAACAAC CTCAATGACG AAGACGTCTC TATCCTGATG  
120

GATCGAAACC TTCGACTTCC AAACCTGGAG AGCTTCGTAA GGGCTGTCAA GAACTTAGAA  
180

AATGCATCAG GTATTGAGGC AATTCTTCGT AATCTCCAAC CATGTCTGCC CTCTGCCACG  
240

GCCGCACCCCT CTCGACATCC AATCATCATC AAGGCAGGTG ACTGGCAAGA ATTCCGGGAA  
300

AAACTGACGT TCTATCTGGT TACCCTTGAG CAAGCGCAGG AACAAACAGTA CGTAGAGGGC  
360

GGTGGAGGCT CCCCGGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG  
420

TCTAAAGAAT CTCATAAATC TCCAAACATG GCTTTAGGCC CTGCCAGCTC CCTGCCCCAG  
480

AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC AGGGCGATGG CGCAGCGCTC  
540

CAGGAGAAGC TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA  
600

CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG  
660

GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC  
720

CTGGAAGGGA TATCCCCCGA GTTGGGTCCC ACCTTGGACA CACTGCAGCT GGACGTCGCC  
780

GACTTTGCCA CCACCATCTG GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG  
840

CCCACCCAGG GTGCCATGCC GGCCTTCGCC TCTGCTTTCC AGCGCCGGGC AGGAGGGGTC  
900

CTGGTTGCTA GCCATCTGCA GAGCTTCCTG GAGGTGTCGT ACCGCGTTCT ACGCCACCTT  
960

GCGCAGCCCG ACATGGCTAC ACCAACGTAC TCCATGGCTA ACTGCTCTAT AATGATCGAT  
1020

GAAATTATAC ATCACTTAAA GAGACCACCT GCACCTTTGC TGGACCCGAA CAACCTCAAT  
1080

GACGAAGACG TCTCTATCCT GATGGATCGA AACCTTCGAC TTCCAAACCT GGAGAGCTTC  
1140

GTAAGGGCTG TCAAGAACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC  
1200

CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA  
1260

GGTGACTGGC AAGAATTCCG GGAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG  
1320

CAGGAACAAC AGTACGTAGA GGGCGGTGGA GGCTCCCCGG GTGAACCGTC TGGTCCAATC  
1380

TCTACTATCA ACCCGTCTCC TCCGTCTAAA GAATCTCATA AATCTCCAAA CATGGCTCAG  
1440

AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC AGGGCGATGG CGCAGCGCTC  
1500

CAGGAGAAGC TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA  
1560

CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG  
1620

GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC  
1680

CTGGAAGGGA TATCCCCCGA GTTGGGTCCC ACCTTGACA CACTGCAGCT GGACGTCGCC  
1740

GACTTTGCCA CCACCATCTG GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG  
1800

CCCACCCAGG GTGCCATGCC GGCCTTCGCC TCTGCTTTCC AGCGCCGGGC AGGAGGGGTC  
1860

CTGGTTGCTA GCCATCTGCA GAGCTTCCTG GAGGTGTCGT ACCGCGTTCT ACGCCACCTT  
1920

GCGCAGCCCG ACATGGCTAC ACCATTAGGC CCTGCCAGCT CCCTGCCCAC GTACTCCATG  
1980

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
2040

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA TCGAAACCTT

2100

CGACTTCCAA ACCTGGAGAG CTTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
2160

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCTCT  
2220

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC  
2280

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
2340

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
2400

CATAAATCTC CAAACATGGC TTTCTGCTC AAGTCTTTAG AGCAAGTGAG GAAGATCCAG  
2460

GGCGATGGCG CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG CCACCCCGAG  
2520

GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCTGCCCC  
2580

AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCTCTAC  
2640

CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCGAGT TGGGTCCCAC CTTGGACACA  
2700

CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA  
2760

ATGGCCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG CCTTCGCCTC TGCTTTCCAG  
2820

CGCCGGGCAG GAGGGGTCTT GGTGCTAGC CATCTGCAGA GCTTCCTGGA GGTGTCGTAC  
2880

CGCGTTCTAC GCCACCTTGC GCAGCCCGAC ATGGCTACAC CATTAGGCCC TGCCAGCTCC  
2940

CTGCCCCAGA GCACGTACTC CATGGCTAAC TGCTCTATAA TGATCGATGA AATTATACAT  
3000

CACTTAAAGA GACCACCTGC ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC  
3060

TCTATCCTGA TGGATCGAAA CCTTCGACTT CCAAACCTGG AGAGCTTCGT AAGGGCTGTC  
3120

AAGAACTTAG AAAATGCATC AGGTATTGAG GCAATTCTTC GTAATCTCCA ACCATGTCTG  
3180

CCCTCTGCCA CGGCCGCACC CTCTCGACAT CCAATCATCA TCAAGGCAGG TGAAGGCAA  
3240

GAATTCCGGG AAAAAGTAC GTTCTATCTG GTTACCCTTG AGCAAGCGCA GGAACAACAG  
3300

TACGTAGAGG GCGGTGGAGG CTCCCCGGGT GAACCGTCTG GTCCAATCTC TACTATCAAC  
3360

CCGTCTCCTC CGTCTAAAGA ATCTCATAAA TCTCCAAACA TGGCTGAGCA AGTGAGGAAG  
3420

ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC  
3480

CCCGAGGAGC TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC  
3540

TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG CGGCCTTTTC  
3600

CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC CCGAGTTGGG TCCCACCTTG  
3660

GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA GATGGAAGAA  
3720

CTGGGAATGG CCCCTGCCCT GCAGCCCACC CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT  
3780

TTCCAGCGCC GGGCAGGAGG GGTCTGGTT GCTAGCCATC TGCAGAGCTT CCTGGAGGTG  
3840

TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCGACATGG CTACACCATT AGGCCCTGCC  
3900

AGCTCCCTGC CCCAGAGCTT CCTGCTCAAG TCTTTAACGT ACTCCATGGC TAACTGCTCT  
3960

ATAATGATCG ATGAAATTAT ACATCACTTA AAGAGACCAC CTGCACCTTT GCTGGACCCG  
4020

AACAACCTCA ATGACGAAGA CGTCTCTATC CTGATGGATC GAAACCTTCG ACTTCCAAAC  
4080

CTGGAGAGCT TCGTAAGGGC TGTCAAGAAC TTAGAAAATG CATCAGGTAT TGAGGCAATT  
4140

CTTCGTAATC TCCAACCATG TCTGCCCTCT GCCACGGCCG CACCCTCTCG ACATCCAATC  
4200

ATCATCAAGG CAGGTGACTG GCAAGAATTC CGGGAAAAAC TGACGTTCTA TCTGGTTACC  
4260

CTTGAGCAAG CGCAGGAACA ACAGTACGTA GAGGGCGGTG GAGGCTCCCC GGGTGAACCG  
4320

TCTGGTCCAA TCTCTACTAT CAACCCGTCT CCTCCGTCTA AAGAATCTCA TAAATCTCCA  
4380

AACATGGCTC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC  
4440

AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCTCTAC  
4500

CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCGAGT TGGGTCCCAC CTTGGACACA  
4560

CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA  
4620

ATGGCCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG CCTTCGCCTC TGCTTTCCAG  
4680

CGCCGGGCAG GAGGGGTCCT GGTGCTAGC CATCTGCAGA GCTTCCTGGA GGTGTCGTAC  
4740

CGCGTTCTAC GCCACCTTGC GCAGCCCGAC ATGGCTACAC CATTAGGCCC TGCCAGCTCC  
4800

CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA GAGCAAGTGA GGAAGATCCA GGGCGATGGC  
4860

GCAGCGCTCC AGGAGAAGCT GTGTGCCACC TACAAGCTGT GCCACCCCGA GGAGCTGGTG  
4920

ACGTA CTCCA TGGCTAACTG CTCTATAATG ATCGATGAAA TTATACATCA CTTAAAGAGA  
4980

CCACCTGCAC CTTTGCTGGA CCCGAACAAC CTCAATGACG AAGACGTCTC TATCCTGATG  
5040

GATCGAAACC TTCGACTTCC AAACCTGGAG AGCTTCGTAA GGGCTGTCAA GAACTTAGAA  
5100

AATGCATCAG GTATTGAGGC AATTCTTCGT AATCTCCAAC CATGTCTGCC CTCTGCCACG  
5160

GCCGCACCTT CTCGACATCC AATCATCATC AAGGCAGGTG ACTGGCAAGA ATTCCGGGAA  
5220

AAACTGACGT TCTATCTGGT TACCCTTGAG CAAGCGCAGG AACAAACAGTA CGTAGAGGGC  
5280

GGTGGAGGCT CCCCGGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG  
5340

TCTAAAGAAT CTCATAAATC TCCAAACATG GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC  
5400

CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA CCAGGGGCTC  
5460

CTGCAGGCCC TGAAGGGAT ATCCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG  
5520

GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCCT  
5580

GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA  
5640

GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA  
5700

CGCCACCTTG CGCAGCCCGA CATGGCTACA CCATTAGGCC CTGCCAGCTC CCTGCCCCAG

5760

AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC AGGGCGATGG CGCAGCGCTC  
5820

CAGGAGAAGC TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA  
5880

CACTCTCTGG GCATCCCCTG GGCTACGTAC TCCATGGCTA ACTGCTCTAT AATGATCGAT  
5940

GAAATTATAC ATCACTTAAA GAGACCACCT GCACCTTTGC TGGACCCGAA CAACCTCAAT  
6000

GACGAAGACG TCTCTATCCT GATGGATCGA AACCTTCGAC TTCCAAACCT GGAGAGCTTC  
6060

GTAAGGGCTG TCAAGAACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC  
6120

CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA  
6180

GGTGACTGGC AAGAATTCCG GGAAAACTG ACGTTCTATC TGGTTACCTT TGAGCAAGCG  
6240

CAGGAACAAC AGTACGTAGA GGGCGGTGGA GGCTCCCCGG GTGAACCGTC TGGTCCAATC  
6300

TCTACTATCA ACCCGTCTCC TCCGTCTAAA GAATCTCATA AATCTCCAAA CATGGCTCAG  
6360

GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG  
6420

CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG  
6480

CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGAATGGCC  
6540

CCTGCCCTGC AGCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG  
6600

GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT  
6660

CTACGCCACC TTGCGCAGCC CGACATGGCT ACACCATTAG GCCCTGCCAG CTCCCTGCCC  
6720

CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG  
6780

CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC  
6840

GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCAC GTACTCCATG  
6900

GCTAACTGCT CTATAATGAT CGATGAAATT ATACATCACT TAAAGAGACC ACCTGCACCT  
6960

TTGCTGGACC CGAACAACCT CAATGACGAA GACGTCTCTA TCCTGATGGA TCGAAACCTT  
7020

CGACTTCCAA ACCTGGAGAG CTTCTGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT  
7080

ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC CGCACCCCTCT  
7140

CGACATCCAA TCATCATCAA GGCAGGTGAC TGGCAAGAAT TCCGGGAAAA ACTGACGTTC  
7200

TATCTGGTTA CCCTTGAGCA AGCGCAGGAA CAACAGTACG TAGAGGGCGG TGGAGGCTCC  
7260

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT  
7320

CATAAATCTC CAAACATGGC TCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC  
7380

CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC  
7440

ACCTTGACAA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG  
7500

GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCACCCAGG GTGCCATGCC GGCCTTCGCC  
7560

TCTGCTTTCC AGCGCCGGGC AGGAGGGGTC CTGGTTGCTA GCCATCTGCA GAGCTTCCTG  
7620

GAGGTGTCGT ACCGCGTTCT ACGCCACCTT GCGCAGCCCG ACATGGCTAC ACCATTAGGC  
7680

CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTCTT TAGAGCAAGT GAGGAAGATC  
7740

CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA CCTACAAGCT GTGCCACCCC  
7800

GAGGAGCTGG TGCTGCTCGG ACACTCTCTG GGCATCCCCCT GGGCTCCCCCT GAGCTCCTGC  
7860

CCCAGCCAGG CCACGTACTC CATGGCTAAC TGCTCTATAA TGATCGATGA AATTATACAT  
7920

CACTTAAAGA GACCACCTGC ACCTTTGCTG GACCCGAACA ACCTCAATGA CGAAGACGTC  
7980

TCTATCCTGA TGGATCGAAA CCTTCGACTT CCAAACCTGG AGAGCTTCGT AAGGGCTGTC  
8040

AAGAACTTAG AAAATGCATC AGGTATTGAG GCAATTCTTC GTAATCTCCA ACCATGTCTG  
8100

CCCTCTGCCA CGGCCGCACC CTCTCGACAT CCAATCATCA TCAAGGCAGG TGACTGGCAA  
8160

GAATTCCGGG AAAAAGTAC GTTCTATCTG GTTACCCTTG AGCAAGCGCA GGAACAACAG  
8220

TACGTAGAGG GCGGTGGAGG CTCCCCGGGT GAACCGTCTG GTCCAATCTC TACTATCAAC  
8280

CCGTCTCCTC CGTCTAAAGA ATCTCATAAA TCTCCAAACA TGGCTCTGGC AGGCTGCTTG  
8340

AGCCAAGTCC ATAGCGGCCT TTTCTCTAC CAGGGGCTCC TGCAGGCCCT GGAAGGGATA  
8400

TCCCCGAGT TGGGTCCCAC CTTGGACACA CTGCAGCTGG ACGTCGCCGA CTTTGCCACC  
8460

ACCATCTGGC AGCAGATGGA AGAACTGGGA ATGGCCCCTG CCCTGCAGCC CACCCAGGGT  
8520

GCCATGCCGG CCTTCGCCTC TGCTTTCCAG CGCCGGGCAG GAGGGGTCCT GGTGCTAGC  
8580

CATCTGCAGA GCTTCCTGGA GGTGTCGTAC CGCGTTCTAC GCCACCTTGC GCAGCCCGAC  
8640

ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA  
8700

GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC  
8760

TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG  
8820

GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGACGT ACTCCATGGC TAACTGCTCT  
8880

ATAATGATCG ATGAAATTAT ACATCACTTA AAGAGACCAC CTGCACCTTT GCTGGACCCG  
8940

AACAACCTCA ATGACGAAGA CGTCTCTATC CTGATGGATC GAAACCTTCG ACTTCCAAAC  
9000

CTGGAGAGCT TCGTAAGGGC TGTCAAGAAC TTAGAAAATG CATCAGGTAT TGAGGCAATT  
9060

CTTCGTAATC TCCAACCATG TCTGCCCTCT GCCACGGCCG CACCCTCTCG ACATCCAATC  
9120

ATCATCAAGG CAGGTGACTG GCAAGAATTC CGGGAAAAAC TGACGTTCTA TCTGGTTACC  
9180

CTTGAGCAAG CGCAGGAACA ACAGTACGTA GAGGGCGGTG GAGGCTCCCC GGGTGAACCG  
9240

TCTGGTCCAA TCTCTACTAT CAACCCGTCT CCTCCGTCTA AAGAATCTCA TAAATCTCCA  
9300

AACATGGCTG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC  
9360

TTGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC

9420

TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCGACAT GGCTACACCA  
9480

TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG  
9540

AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC  
9600

CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC  
9660

TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT  
9720

TTCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC  
9780

TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA  
9840

ACGTACTCCA TGGCTAACTG CTCTATAATG ATCGATGAAA TTATACATCA CTTAAAGAGA  
9900

CCACCTGCAC CTTTGCTGGA CCCGAACAAC CTCAATGACG AAGACGTCTC TATCCTGATG  
9960

GATCGAAACC TTCGACTTCC AAACCTGGAG AGCTTCGTAA GGGCTGTCAA GAACTTAGAA  
10020

AATGCATCAG GTATTGAGGC AATTCTTCGT AATCTCCAAC CATGTCTGCC CTCTGCCACG  
10080

GCCGCACCTT CTCGACATCC AATCATCATC AAGGCAGGTG ACTGGCAAGA ATTCCGGGAA  
10140

AAACTGACGT TCTATCTGGT TACCCTTGAG CAAGCGCAGG AACAAACAGTA CGTAGAGGGC  
10200

GGTGGAGGCT CCCCGGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG  
10260

TCTAAAGAAT CTCATAAATC TCCAAACATG GCTGGAATGG CCCCTGCCCT GCAGCCCACC  
10320

CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT TTCCAGCGCC GGGCAGGAGG GGTCTTGTT  
10380

GCTAGCCATC TGCAGAGCTT CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG  
10440

CCCGACATGG CTACACCATT AGGCCCTGCC AGCTCCCTGC CCCAGAGCTT CTGCTCAAG  
10500

TCTTTAGAGC AAGTGAGGAA GATCCAGGGC GATGGCGCAG CGCTCCAGGA GAAGCTGTGT  
10560

GCCACCTACA AGCTGTGCCA CCCCAGGAG CTGGTGCTGC TCGGACACTC TCTGGGCATC  
10620

CCCTGGGCTC CCCTGAGCTC CTGCCCCAGC CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC  
10680

CAACTCCATA GCGGCCTTTT CCTCTACCAG GGGCTCCTGC AGGCCCTGGA AGGGATATCC  
10740

CCCAGATTGG GTCCACCTT GGACACACTG CAGCTGGACG TCGCCGACTT TGCCACCACC  
10800

ATCTGGCAGC AGATGGAAGA ACTGACGTAC TCCATGGCTA ACTGCTCTAT AATGATCGAT  
10860

GAAATTATAC ATCACTTAAA GAGACCACCT GCACCTTTGC TGGACCCGAA CAACCTCAAT  
10920

GACGAAGACG TCTCTATCCT GATGGATCGA AACCTTCGAC TTCCAAACCT GGAGAGCTTC  
10980

GTAAGGGCTG TCAAGAACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC  
11040

CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA  
11100

GGTGA CTGGC AAGAATTCCG GGAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG  
11160

CAGGAACAAC AGTACGTAGA GGGCGGTGGA GGCTCCCCGG GTGAACCGTC TGGTCCAATC  
11220

TCTACTATCA ACCCGTCTCC TCCGTCTAAA GAATCTCATA AATCTCCAAA CATGGCTAGC  
11280

TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCGACAT GGCTACACCA  
11340

TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC TTCTTGCTCA AGTCTTTAGA GCAAGTGAGG  
11400

AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC  
11460

CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC  
11520

TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT  
11580

TTCCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC  
11640

TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA  
11700

GAACTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTGCGCTCT  
11760

GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC ATCTGCAG  
11808

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG  
480

AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC  
540

CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC  
600

TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT  
660

TTCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC  
720

TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA  
780

GAACTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTGCCTCT  
840

GCTTTCCAGC GCCGGGCAGG AGGGGTCTTG GTTGCTAGCC ATCTGCAGAG CTTCTGGAG  
900

GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCGACA TGGCTACACC ATTAGGCCCT  
960

GCCAGCTCCC TGCCC  
975

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TTCATAAAT CTCCAAACAT GGCTCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG  
480

AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC  
540

CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC  
600

TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT  
660

TTCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC  
720

TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA  
780

GAACTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTGCCTCT  
840

GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC ATCTGCAGAG CTTCTGGAG  
900

GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCGACA TGGCTACACC ATTAGGCCCT  
960

GCCAGCTCCC TGCCC  
975

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTGAGCAA GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG  
480

CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC  
540

GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG  
600

CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG  
660

GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC  
720

GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG  
780

CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG  
840

GTCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC  
900

CTTGCGCAGC CCGACATGGC TACACCATTA GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC  
960

CTGCTCAAGT CTTTA  
975

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC  
480

CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA ACTCCATAGC  
540

GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT  
600

CCCACCTTGG ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG  
660

ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC  
720

GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC  
780

CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCGACATGGC TACACCATTA  
840

GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG  
900

ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC  
960

CCCGAGGAGC TGGTG  
975

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 975 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG  
480

GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC  
540

CTGGAAGGGA TATCCCCCGA GTTGGGTCCC ACCTTGGACA CACTGCAGCT GGACGTCGCC  
600

GACTTTGCCA CCACCATCTG GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG  
660

CCCACCCAGG GTGCCATGCC GGCCTTCGCC TCTGCTTTCC AGCGCCGGGC AGGAGGGGTC  
720

CTGGTTGCTA GCCATCTGCA GAGCTTCCTG GAGGTGTCGT ACCGCGTTCT ACGCCACCTT  
780

GCGCAGCCCG ACATGGCTAC ACCATTAGGC CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG  
840

CTCAAGTCTT TAGAGCAAGT GAGGAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG  
900

CTGTGTGCCA CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG AACTCTCTG  
960

GGCATCCCCCT GGGCT  
975

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC  
480

CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG  
540

TTGGGTCCCA CCTTGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG  
600

CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG  
660

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG  
720

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCGA CATGGCTACA  
780

CCATTAGGCC CTGCCAGCTC CCTGCCCCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG  
840

AGGAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG  
900

TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG  
960

AGCTCCTGCC CCAGC  
975

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300

TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360

TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420

TCTCATAAAT CTCCAAACAT GGCTCTGCAG CTGGCAGGCT GCTTGAGCCA ACTCCATAGC  
480

GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT  
540

CCCACCTTGG ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG  
600

ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC  
660

GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCTTGTTG CTAGCCATCT GCAGAGCTTC  
720

CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCGACATGGC TACACCATTA  
780

GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG  
840

ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC  
900

CCCGAGGAGC TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC  
960

TGCCCCAGCC AGGCC  
975

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 975 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60

CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
 120  
 CTTCTGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
 300  
 TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
 360  
 TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
 420  
 TCTCATAAAT CTCCAAACAT GGCTCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT  
 480  
 TTCCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC  
 540  
 TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA  
 600  
 GAACTGGGAA TGGCCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTCT  
 660  
 GCTTTCCAGC GCCGGGCAGG AGGGGTCTTG GTTGCTAGCC ATCTGCAGAG CTTCTGGAG  
 720  
 GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCGACA TGGCTACACC ATTAGGCCCT  
 780  
 GCCAGCTCCC TGCCCCAGAG CTTCTGCTC AAGTCTTTAG AGCAAGTGAG GAAGATCCAG  
 840  
 GGCATGGCG CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG CCACCCCGAG  
 900  
 GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC  
 960  
 AGCCAGGCCC TGCAG  
 975

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 975 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60  
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
120  
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180  
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240  
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300  
TTCTATCTGG TTACCCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360  
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420  
TCTCATAAAT CTCCAAACAT GGCTGAACTG GGAATGGCCC CTGCCCTGCA GCCCACCAG  
480  
GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT  
540  
AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC TACGCCACCT TGCGCAGCCC  
600  
GACATGGCTA CACCATTAGG CCCTGCCAGC TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT  
660  
TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC  
720  
ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG GACACTCTCT GGGCATCCCC  
780  
TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA  
840  
CTCCATAGCG GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCCCC  
900  
GAGTTGGGTC CCACCTTGA CACACTGCAG CTGGACGTCG CCGACTTTGC CACCACCATC  
960  
TGGCAGCAGA TGGAA  
975

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 975 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA  
60  
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC  
120  
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA  
180  
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC  
240  
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG  
300  
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC  
360  
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA  
420  
TCTCATAAAT CTCCAAACAT GGCTGGAATG GCCCCTGCCC TGCAGCCCAC CCAGGGTGCC  
480  
ATGCCGGCCT TCGCCTCTGC TTTCCAGCGC CGGGCAGGAG GGGTCCTGGT TGCTAGCCAT  
540  
CTGCAGAGCT TCCTGGAGGT GTCGTACCGC GTTCTACGCC ACCTTGCGCA GCCCCACATG  
600  
GCTACACCAT TAGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG  
660  
CAAGTGAGGA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC  
720  
AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT  
780  
CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT  
840  
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCAGATTG  
900  
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG  
960  
CAGATGGAAG AACTG  
975

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 975 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

```
ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA
60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGATCGAAAC
120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA
180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC
240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC
360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA
420
TCTCATAAAT CTCCAAACAT GGCTAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC
480
CTTGCGCAGC CCGACATGGC TACACCATTA GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC
540
CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG
600
AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT
660
CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC
720
TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA
780
GGGATATCCC CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT
840
GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCACC
900
CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT TTCCAGCGCC GGGCAGGAGG GGTCTTGGTT
```

960

GCTAGCCATC TGCAG

975

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Asn | Met | Ala | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | 225 | 230 | 235 | 240 |
| Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | 245 | 250 | 255 |     |
| Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | 260 | 265 | 270 |     |
| Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | 275 | 280 | 285 |     |
| Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | 290 | 295 | 300 |     |
| Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | 305 | 310 | 315 | 320 |
| Asp | Met | Ala | Thr | Pro |     |     |     |     |     |     |     |     |     |     |     | 325 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | 1   | 5   | 10  | 15 |
| Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | 20  | 25  | 30  |    |
| Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | 35  | 40  | 45  |    |
| Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | 50  | 55  | 60  |    |
| Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | 65  | 70  | 75  | 80 |
| Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | 85  | 90  | 95  |    |
| Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | 100 | 105 | 110 |    |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | 115 | 120 | 125 |    |



| 35                                                              | 40  | 45  |
|-----------------------------------------------------------------|-----|-----|
| Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala |     |     |
| 50                                                              | 55  | 60  |
| Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro |     |     |
| 65                                                              | 70  | 75  |
| Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg |     |     |
|                                                                 | 85  | 90  |
| Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln |     |     |
|                                                                 | 100 | 105 |
| Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro |     |     |
|                                                                 | 115 | 120 |
| Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser |     |     |
|                                                                 | 130 | 135 |
| Pro Asn Met Ala Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile |     |     |
|                                                                 | 145 | 150 |
| Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys |     |     |
|                                                                 | 165 | 170 |
| Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile |     |     |
|                                                                 | 180 | 185 |
| Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala |     |     |
|                                                                 | 195 | 200 |
| Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu |     |     |
|                                                                 | 210 | 215 |
| Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp |     |     |
|                                                                 | 225 | 230 |
| Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln |     |     |
|                                                                 | 245 | 250 |
| Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala |     |     |
|                                                                 | 260 | 265 |
| Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu |     |     |
|                                                                 | 275 | 280 |
| Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu |     |     |
|                                                                 | 290 | 295 |
| Arg His Leu Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser |     |     |
|                                                                 | 305 | 310 |
| Ser Leu Pro Gln Ser                                             |     |     |
|                                                                 | 325 |     |

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Pro | Asn | Met | Ala | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Met | Ala | Thr | Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Leu | Lys | Ser | Leu |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Asn | Met | Ala | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu |

|                                                                 |     |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|
|                                                                 | 180 |     | 185 |     | 190 |
| Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu | 195 |     | 200 |     | 205 |
| Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu | 210 |     | 215 |     | 220 |
| Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe | 225 |     | 230 |     | 235 |
| Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His |     | 245 |     | 250 | 255 |
| Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala |     | 260 |     | 265 | 270 |
| Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln |     | 275 |     | 280 | 285 |
| Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp |     | 290 |     | 295 | 300 |
| Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His |     | 305 |     | 310 | 315 |
| Pro Glu Glu Leu Val                                             |     | 325 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

|                                                                 |   |    |    |    |
|-----------------------------------------------------------------|---|----|----|----|
| Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys | 1 | 5  | 10 | 15 |
| Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp |   | 20 | 25 | 30 |
| Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser |   | 35 | 40 | 45 |
| Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala |   | 50 | 55 | 60 |
| Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro |   | 65 | 70 | 75 |
| Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg |   | 85 | 90 | 95 |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | 1   | 5   | 10  | 15  |
| Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | 20  | 25  | 30  |     |
| Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | 35  | 40  | 45  |     |
| Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | 50  | 55  | 60  |     |
| Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | 65  | 70  | 75  | 80  |
| Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | 85  | 90  | 95  |     |
| Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | 100 | 105 | 110 |     |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | 115 | 120 | 125 |     |
| Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | 130 | 135 | 140 |     |
| Pro | Asn | Met | Ala | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | 145 | 150 | 155 | 160 |
| His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | 165 | 170 | 175 |     |
| Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | 180 | 185 | 190 |     |
| Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | 195 | 200 | 205 |     |
| Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | 210 | 215 | 220 |     |
| Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | 225 | 230 | 235 | 240 |
| Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | 245 | 250 | 255 |     |
| Asp | Met | Ala | Thr | Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | 260 | 265 | 270 |     |
| Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | 275 | 280 | 285 |     |
| Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | 290 | 295 | 300 |     |
| Glu | Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | 305 | 310 | 315 | 320 |
| Ser | Ser | Cys | Pro | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:278:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | 1   | 5   | 10  | 15  |
| Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | 20  | 25  | 30  |     |
| Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | 35  | 40  | 45  |     |
| Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala | 50  | 55  | 60  |     |
| Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro | 65  | 70  | 75  | 80  |
| Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg | 85  | 90  | 95  |     |
| Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln | 100 | 105 | 110 |     |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro | 115 | 120 | 125 |     |
| Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser | 130 | 135 | 140 |     |
| Pro | Asn | Met | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | 145 | 150 | 155 | 160 |
| Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | 165 | 170 | 175 |     |
| Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | 180 | 185 | 190 |     |
| Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | 195 | 200 | 205 |     |
| Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | 210 | 215 | 220 |     |
| Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe | 225 | 230 | 235 | 240 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Asp | Met |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Ala | Thr | Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Cys | Pro | Ser | Gln | Ala |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:279:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Asn | Met | Ala | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | 145 | 150 | 155 | 160 |
| Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | 165 | 170 | 175 |     |
| Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | 180 | 185 | 190 |     |
| Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | 195 | 200 | 205 |     |
| Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg | 210 | 215 | 220 |     |
| Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | 225 | 230 | 235 | 240 |
| Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Asp | Met | Ala | Thr | 245 | 250 | 255 |     |
| Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu | Lys | Ser | 260 | 265 | 270 |     |
| Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | 275 | 280 | 285 |     |
| Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | 290 | 295 | 300 |     |
| Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | 305 | 310 | 315 | 320 |
| Ser | Gln | Ala | Leu | Gln |     |     |     |     |     |     |     |     |     |     |     | 325 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |    |    |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Met | Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys | 1  | 5  | 10 | 15 |
| Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp | 20 | 25 | 30 |    |
| Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser | 35 | 40 | 45 |    |
| Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala |    |    |    |    |

| 50                                                                                 | 55 | 60 |
|------------------------------------------------------------------------------------|----|----|
| Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro<br>65 70 75 80     |    |    |
| Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg<br>85 90 95        |    |    |
| Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln<br>100 105 110     |    |    |
| Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro<br>115 120 125     |    |    |
| Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser<br>130 135 140     |    |    |
| Pro Asn Met Ala Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln<br>145 150 155 160 |    |    |
| Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly<br>165 170 175     |    |    |
| Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg<br>180 185 190     |    |    |
| Val Leu Arg His Leu Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro<br>195 200 205     |    |    |
| Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val<br>210 215 220     |    |    |
| Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala<br>225 230 235 240 |    |    |
| Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser<br>245 250 255     |    |    |
| Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu<br>260 265 270     |    |    |
| Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr<br>275 280 285     |    |    |
| Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro<br>290 295 300     |    |    |
| Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile<br>305 310 315 320 |    |    |
| Trp Gln Gln Met Glu<br>325                                                         |    |    |

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Cys | Ser | Ile | Met | Ile | Asp | Glu | Ile | Ile | His | His | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Pro | Pro | Ala | Pro | Leu | Leu | Asp | Pro | Asn | Asn | Leu | Asn | Asp | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ser | Ile | Leu | Met | Asp | Arg | Asn | Leu | Arg | Leu | Pro | Asn | Leu | Glu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Val | Arg | Ala | Val | Lys | Asn | Leu | Glu | Asn | Ala | Ser | Gly | Ile | Glu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Arg | Asn | Leu | Gln | Pro | Cys | Leu | Pro | Ser | Ala | Thr | Ala | Ala | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Arg | His | Pro | Ile | Ile | Ile | Lys | Ala | Gly | Asp | Trp | Gln | Glu | Phe | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Lys | Leu | Thr | Phe | Tyr | Leu | Val | Thr | Leu | Glu | Gln | Ala | Gln | Glu | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Tyr | Val | Glu | Gly | Gly | Gly | Gly | Ser | Pro | Gly | Glu | Pro | Ser | Gly | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ser | Thr | Ile | Asn | Pro | Ser | Pro | Pro | Ser | Lys | Glu | Ser | His | Lys | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Asn | Met | Ala | Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | His | Leu | Ala | Gln | Pro | Asp | Met | Ala | Thr | Pro | Leu | Gly | Pro | Ala | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu  
 290 295 300  
 Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln  
 305 310 315 320  
 Gln Met Glu Glu Leu  
 325

(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 325 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
 20 25 30  
 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
 35 40 45  
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro  
 115 120 125  
 Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser  
 130 135 140  
 Pro Asn Met Ala Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His  
 145 150 155 160  
 Leu Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu  
 165 170 175  
 Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln  
 180 185 190  
 Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu

| 195                                                             | 200                                 | 205     |
|-----------------------------------------------------------------|-------------------------------------|---------|
| Cys His Pro Glu Glu Leu Val                                     | Leu Leu Gly His Ser Leu Gly Ile Pro |         |
| 210                                                             | 215                                 | 220     |
| Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly |                                     |         |
| 225                                                             | 230                                 | 235 240 |
| Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu |                                     |         |
|                                                                 | 245                                 | 250 255 |
| Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr |                                     |         |
|                                                                 | 260                                 | 265 270 |
| Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met |                                     |         |
|                                                                 | 275                                 | 280 285 |
| Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met |                                     |         |
|                                                                 | 290                                 | 295 300 |
| Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val |                                     |         |
| 305                                                             | 310                                 | 315 320 |
| Ala Ser His Leu Gln                                             |                                     |         |
|                                                                 | 325                                 |         |

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 7
  - (D) OTHER INFORMATION: /note= "Xaa at position 7 is Ser or Ala;"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 112
  - (D) OTHER INFORMATION: /note= "Xaa at position 112 is deleted or Leu, Ala, Val, Ile, Pro, Phe, Trp, or Met;"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 113
  - (D) OTHER INFORMATION: /note= "Xaa at position 113 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp, or Met;"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 114
  - (D) OTHER INFORMATION: /note= "Xaa at position 114 is deleted or Pro, Phe, Ala, Val, Leu, Ile, Trp, or Met;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 115  
 (D) OTHER INFORMATION: /note= "Xaa at position 115 is deleted or Gln, Gly, Ser, Thr, Tyr, or Asn;"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 151  
 (D) OTHER INFORMATION: /note= "Xaa at position 151 is Ser or Ala;"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Ala | Pro | Pro | Ala | Xaa | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly | Gln |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Leu | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln | Xaa |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Xaa | Xaa | Xaa | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Gly | Gly | Ser | Thr | Leu | Xaa | Val | Arg |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 162 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Met Ala Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu

|     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     | 5   |     | 10  |     | 15  |     |
| Ser | Phe | Gln | His | Leu | Leu | Arg | Gly |
|     |     | 20  |     |     |     | 25  |     |
| Lys | Val | Arg | Phe | Leu | Met | Leu | Val |
|     |     |     |     |     | 30  |     |     |
| Gly | Gly | Ser | Thr | Leu | Ala | Val | Arg |
|     |     | 35  |     |     |     | 40  |     |
| Glu | Phe | Gly | Gly | Asn | Met | Ala | Ser |
|     |     |     |     | 45  |     |     |     |
| Pro | Ala | Pro | Pro | Ala | Ala | Asp | Leu |
|     | 50  |     |     |     |     | 55  |     |
| Val | Leu | Ser | Lys | Leu | Leu | Arg |     |
|     |     | 60  |     |     |     |     |     |
| Asp | Ser | His | Val | Leu | His | Ser | Arg |
|     | 65  |     |     |     | 70  |     |     |
| Leu | Ser | Gln | Cys | Pro | Glu | Val | His |
|     |     | 75  |     |     |     |     | 80  |
| Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu |
|     |     |     | 85  |     |     |     |     |
| Pro | Ala | Val | Asp | Phe | Ser | Leu | Gly |
|     |     | 90  |     |     |     | 95  |     |
| Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu |
|     |     |     | 100 |     |     |     |     |
| Thr | Lys | Ala | Gln | Asp | Ile | Leu | Gly |
|     |     |     |     |     | 110 |     |     |
| Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly |
|     |     | 115 |     |     |     | 120 |     |
| Val | Met | Ala | Ala | Arg | Gly | Gln | Leu |
|     |     |     |     | 125 |     |     |     |
| Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu |
|     | 130 |     |     |     |     | 135 |     |
| Leu | Leu | Gly | Gln | Leu | Ser | Gly | Gln |
|     |     |     |     | 140 |     |     |     |
| Val |     |     |     |     |     |     |     |
| Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln |
|     | 145 |     |     |     | 150 |     |     |
| Ser | Leu | Leu | Gly | Thr | Gln | Leu | Pro |
|     |     |     | 155 |     |     |     | 160 |
| Pro | Gln |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 162 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Pro | Thr | Cys | Leu | Ser | Ser | Leu | Leu | Gly | Gln | Leu | Ser | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Val | Arg | Leu | Leu | Leu | Gly | Ala | Leu | Gln | Ser | Leu | Leu | Gly | Thr | Gln |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Pro | Pro | Gln | Gly | Arg | Thr | Thr | Ala | His | Lys | Asp | Pro | Asn | Ala | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Phe | Leu | Ser | Phe | Gln | His | Leu | Leu | Arg | Gly | Lys | Val | Arg | Phe | Leu | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Val | Gly | Gly | Ser | Thr | Leu | Ala | Val | Arg | Glu | Phe | Gly | Gly | Asn | Met |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Pro | Ala | Pro | Pro | Ala | Ala | Asp | Leu | Arg | Val | Leu | Ser | Lys | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Arg | Asp | Ser | His | Val | Leu | His | Ser | Arg | Leu | Ser | Gln | Cys | Pro | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | His | Pro | Leu | Pro | Thr | Pro | Val | Leu | Leu | Pro | Ala | Val | Asp | Phe | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Gly | Glu | Trp | Lys | Thr | Gln | Met | Glu | Glu | Thr | Lys | Ala | Gln | Asp | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Gly | Ala | Val | Thr | Leu | Leu | Leu | Glu | Gly | Val | Met | Ala | Ala | Arg | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 180 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide  
"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Thr | Gly | Gly | Cys | Thr | Gly | Gly | Ala | Cys | Cys | Cys | Ala | Cys | Thr | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Cys | Cys | Thr | Cys | Thr | Cys | Ala | Thr | Cys | Cys | Cys | Thr | Cys | Cys | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Gly | Gly | Gly | Cys | Ala | Gly | Cys | Thr | Thr | Thr | Cys | Thr | Gly | Gly | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Ala | Gly | Gly | Thr | Cys | Cys | Gly | Thr | Cys | Thr | Cys | Cys | Thr | Cys | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Thr | Gly | Gly | Gly | Gly | Cys | Cys | Cys | Thr | Gly | Cys | Ala | Gly | Ala | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Cys | Cys | Thr | Cys | Cys | Thr | Thr | Gly | Gly | Ala | Ala | Cys | Cys | Cys | Ala | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Thr | Thr | Cys | Cys | Thr | Cys | Cys | Ala | Cys | Ala | Gly | Gly | Gly | Cys | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gly | Ala | Cys | Cys | Ala | Cys | Ala | Gly | Cys | Thr | Cys | Ala | Cys | Ala | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Gly | Ala | Thr | Cys | Cys | Cys | Ala | Ala | Thr | Gly | Cys | Cys | Ala | Thr | Cys |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |

Thr Thr Cys Cys Thr Gly Ala Gly Cys Thr Thr Cys Cys Ala Ala Cys  
 145 150 155 160  
 Ala Cys Cys Thr Gly Cys Thr Cys Cys Gly Ala Gly Gly Ala Ala Ala  
 165 170 175  
 Gly Gly Thr Gly  
 180

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

ATGGCTGGCA GGACCACAGC TCACAAGGAT CCAATGCCA TCTTCCTGAG CTTCCAACAC  
 60  
 CTGCTCCGAG GAAAGGTGCG TTTCTGATG CTTGTAGGAG GGTCCACCTT CGCCGTCAGG  
 120  
 GAATTCGGCG GCAACATGGC GTCTCCGGCG CCGCCTGCTG CTGACCTCCG AGTCCTCAGT  
 180  
 AAACTGCTTC GTGACTCCCA TGTCTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTTAC  
 240  
 CCTTTGCCTA CACCTGTCCT GCTGCCTGCT GTGGACTTTA GCTTGGGAGA ATGGAAAACC  
 300  
 CAGATGGAGG AGACCAAGGC ACAGGACATT CTGGGAGCAG TGACCCTTCT GCTGGAGGGA  
 360  
 GTGATGGCAG CACGGGGACA ACTGGGACCC ACTTGCTCTT CATCCCTCCT GGGGCAGCTT  
 420  
 TCTGGACAGG TCCGTCTCCT CCTTGGGGCC CTGCAGAGCC TCCTTGGAAC CCAGCTTCCT  
 480  
 CCACAG  
 486

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGGAAGA TCCAGGGCGA TGGCGCAGCG  
60  
CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC CCGAGGAGCT GGTGCTGCTC  
120  
GGAACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG  
180  
CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG  
240  
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC  
300  
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG  
360  
CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG  
420  
GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC  
480  
CTTGCGCAGC CCGACATGGC TACACCATTA GGCCCTGCCA GCTCCCTGCC C  
531

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 531 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

GAAGTGGGAA TGGCCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTGCGCTCT  
60  
GCTTTCCAGC GCCGGGCAGG AGGGGTCTTG GTTGCTAGCC ATCTGCAGAG CTTCTTGAG  
120  
GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCGACA TGGCTACACC ATTAGGCCCT  
180  
GCCAGCTCCC TGCCCCAGAG CTTCTGCTC AAGTCTTTAG AGCAAGTGAG GAAGATCCAG

240

GGCGATGGCG CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG CCACCCCGAG  
300

GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC  
360

AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCTCTAC  
420

CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCCGAGT TGGGTCCCAC CTTGGACACA  
480

CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA A  
531

(2) INFORMATION FOR SEQ ID NO:290:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 531 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GGAATGGCCC CTGCCCTGCA GCCCACCAG GGTGCCATGC CGGCCTTCGC CTCTGCTTTC  
60

CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG  
120

TACCGCGTTC TACGCCACCT TGCGCAGCCC GACATGGCTA CACCATTAGG CCCTGCCAGC  
180

TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT  
240

GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG  
300

GTGCTGCTCG GAACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG  
360

GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG  
420

CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CAACTGCAG  
480

CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT G  
531

(2) INFORMATION FOR SEQ ID NO:291:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 531 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG  
60  
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC  
120  
TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA  
180  
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG  
240  
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC  
300  
TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCCTGC CCTGCAGCCC  
360  
ACCCAGGGTG CCATGCCGGC CTTGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTTG  
420  
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG  
480  
CAGCCCGACA TGGCTACACC ATTAGGCCCT GCCAGCTCCC TGCCCCAGAG C  
531

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 531 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCGA CATGGCTACA  
60

CCATTAGGCC CTGCCAGCTC CCTGCCCCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG  
120

AGGAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG  
180

TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG  
240

AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC  
300

CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC  
360

ACCTTGACCA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG  
420

GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCACCCAGG GTGCCATGCC GGCCTTCGCC  
480

TCTGCTTTCC AGCGCCGGGC AGGAGGGGTC CTGGTTGCTA GCCATCTGCA G  
531

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCGA CATGGCTACA  
60

CCATTAGGCC CTGCCAGCTC CCTGCCCCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG  
120

AGGAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG  
180

TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG GGCTCCCCTG  
240

AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC  
300

CTTTTCCTCT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC  
360

ACCTTGACCA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG GCAGCAGATG  
420

GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCACCCAGG GTGCCATGCC GGCCTTCGCC  
480

TCTGCTTTCC AGCGCCGGGC AGGAGGGGTC CTGGTTGCTA GCCATCTGCA G  
531

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG  
60

AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC  
120

CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC  
180

TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA TAGCGGCCTT  
240

TTCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC  
300

TTGGACACAC TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA  
360

GAACTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTCGCCTCT  
420

GCTTTCCAGC GCCGGGCAGG AGGGGTCTTG GTTGCTAGCC ATCTGCAGAG CTTCTGGAG  
480

GTGTCGTACC GCGTTCTACG CCACCTTGCG CAGCCCGACA TGGCTACACC A  
531

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

CTGCTCGGAC ACTCTCTGGG CATCCCCTGG GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC  
60  
CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA CCAGGGGCTC  
120  
CTGCAGGCCC TGGAAGGGAT ATCCCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG  
180  
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCCT  
240  
GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA  
300  
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA  
360  
CGCCACCTTG CGCAGCCCGA CATGGCTACA CCATTAGGCC CTGCCAGCTC CCTGCCCCAG  
420  
AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC AGGGCGATGG CGCAGCGCTC  
480  
CAGGAGAAGC TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT G  
531

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT  
60  
AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCAGATTG  
120  
GGTCCCACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC CATCTGGCAG  
180  
CAGATGGAAG AACTGGGAAT GGCCCCTGCC CTGCAGCCCA CCCAGGGTGC CATGCCGGCC  
240  
TTCGCCTCTG CTTTCCAGCG CCGGGCAGGA GGGGTCCTGG TTGCTAGCCA TCTGCAGAGC  
300

TTCCTGGAGG TGTCGTACCG CGTTCTACGC CACCTTGCGC AGCCCGACAT GGCTACACCA  
360

TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG  
420

AAGATCCAGG GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC  
480

CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC T  
531

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC CAACTCCATA GCGGCCTTTT CCTCTACCAG  
60

GGGCTCCTGC AGGCCCTGGA AGGGATATCC CCCGAGTTGG GTCCACCTT GGACACACTG  
120

CAGCTGGACG TCGCCGACTT TGCCACCACC ATCTGGCAGC AGATGGAAGA ACTGGGAATG  
180

GCCCCTGCCC TGCAGCCCAC CCAGGGTGCC ATGCCGGCCT TCGCCTCTGC TTTCCAGCGC  
240

CGGGCAGGAG GGGTCCTGGT TGCTAGCCAT CTGCAGAGCT TCCTGGAGGT GTCGTACCGC  
300

GTTCTACGCC ACCTTGCGCA GCCCGACATG GCTACACCAT TAGGCCCTGC CAGCTCCCTG  
360

CCCCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGGA AGATCCAGGG CGATGGCGCA  
420

GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG  
480

CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG C  
531

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA CCAGGGGCTC  
60  
CTGCAGGCCC TGAAGGGAT ATCCCCGAG TTGGGTCCCA CCTTGGACAC ACTGCAGCTG  
120  
GACGTCGCCG ACTTTGCCAC CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCT  
180  
GCCCTGCAGC CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA  
240  
GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA  
300  
CGCCACCTTG CGCAGCCCGA CATGGCTACA CCATTAGGCC CTGCCAGCTC CCTGCCCCAG  
360  
AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC AGGGCGATGG CGCAGCGCTC  
420  
CAGGAGAAGC TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA  
480  
CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC C  
531

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 531 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG  
60  
GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC  
120  
GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC CCCTGCCCTG

180

CAGCCCACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG  
240

GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC  
300

CTTGCGCAGC CCGACATGGC TACACCATTA GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC  
360

CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG  
420

AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT  
480

CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA G  
531

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |

Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His  
145 150 155 160

Leu Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu  
165 170 175

Pro

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro  
1 5 10 15

Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala  
20 25 30

Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His  
35 40 45

Leu Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu  
50 55 60

Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln  
65 70 75 80

Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu  
85 90 95

Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro  
100 105 110

Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly  
115 120 125

Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu  
130 135 140

Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr  
145 150 155 160

Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met  
165 170 175

Glu

(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Gln | Pro | Asp | Met | Ala | Thr | Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |  |
| Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Glu | Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Gln | Pro | Asp | Met | Ala | Thr | Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |

Ser

(2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp | Met | Ala | Thr | Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Glu | Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gly | Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Met | Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |

Gln

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |  |
| Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Asp | Met | Ala | Thr |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu | Lys | Ser |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |

Leu

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu |  |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg |  |

|                     |                     |                 |         |     |
|---------------------|---------------------|-----------------|---------|-----|
| 130                 |                     | 135             |         | 140 |
| Arg Ala Gly Gly Val | Leu Val Ala Ser His | Leu Gln Ser Phe | Leu Glu |     |
| 145                 | 150                 | 155             | 160     |     |
| Val Ser Tyr Arg Val | Leu Arg His Leu Ala | Gln Pro Asp Met | Ala Thr |     |
|                     | 165                 | 170             | 175     |     |
| Pro                 |                     |                 |         |     |

(2) INFORMATION FOR SEQ ID NO:307:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Asp | Met |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ala | Thr | Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

```
Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
1 5 10 15
Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
20 25 30
Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln
35 40 45
Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
50 55 60
Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
65 70 75 80
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
85 90 95
His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu
100 105 110
Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro
115 120 125
Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly
130 135 140
Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys
145 150 155 160
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
165 170 175
Ala
```

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ala | Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Leu | Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gly | Pro | Thr | Leu | Asp | Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Thr | Ile | Trp | Gln | Gln | Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Pro | Thr | Gln | Gly | Ala | Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Ala | Gly | Gly | Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Ser | Tyr | Arg | Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Asp | Met | Ala | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Leu | Gly | Pro | Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu | Lys | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Glu | Gln | Val | Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Leu | Cys | Ala | Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Gly | His | Ser | Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gln | Leu | Ala | Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Gln | Gly | Leu | Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly |

|                                                                 | 20  | 25  | 30  |
|-----------------------------------------------------------------|-----|-----|-----|
| Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr | 35  | 40  | 45  |
| Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro | 50  | 55  | 60  |
| Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala | 65  | 70  | 75  |
| Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser | 85  | 90  | 95  |
| Tyr Arg Val Leu Arg His Leu Ala Gln Pro Asp Met Ala Thr Pro Leu | 100 | 105 | 110 |
| Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu | 115 | 120 | 125 |
| Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu | 130 | 135 | 140 |
| Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly | 145 | 150 | 155 |
| His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln | 165 | 170 | 175 |
| Ala                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

|                                                                 |    |    |    |    |
|-----------------------------------------------------------------|----|----|----|----|
| Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln | 1  | 5  | 10 | 15 |
| Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr | 20 | 25 | 30 |    |
| Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp | 35 | 40 | 45 |    |
| Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln | 50 | 55 | 60 |    |
| Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly | 65 | 70 | 75 | 80 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Leu | Val | Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Val | Leu | Arg | His | Leu | Ala | Gln | Pro | Asp | Met | Ala | Thr | Pro | Leu | Gly | Pro |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ala | Ser | Ser | Leu | Pro | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Arg | Lys | Ile | Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Thr | Tyr | Lys | Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | Ser |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Leu | Gly | Ile | Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |

Gln

(2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 177 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| His | Leu | Ala | Gln | Pro | Asp | Met | Ala | Thr | Pro | Leu | Gly | Pro | Ala | Ser | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Pro | Gln | Ser | Phe | Leu | Leu | Lys | Ser | Leu | Glu | Gln | Val | Arg | Lys | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gln | Gly | Asp | Gly | Ala | Ala | Leu | Gln | Glu | Lys | Leu | Cys | Ala | Thr | Tyr | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Cys | His | Pro | Glu | Glu | Leu | Val | Leu | Leu | Gly | His | Ser | Leu | Gly | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Pro | Trp | Ala | Pro | Leu | Ser | Ser | Cys | Pro | Ser | Gln | Ala | Leu | Gln | Leu | Ala |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Gly | Cys | Leu | Ser | Gln | Leu | His | Ser | Gly | Leu | Phe | Leu | Tyr | Gln | Gly | Leu |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | Gln | Ala | Leu | Glu | Gly | Ile | Ser | Pro | Glu | Leu | Gly | Pro | Thr | Leu | Asp |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Thr | Leu | Gln | Leu | Asp | Val | Ala | Asp | Phe | Ala | Thr | Thr | Ile | Trp | Gln | Gln |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Glu | Leu | Gly | Met | Ala | Pro | Ala | Leu | Gln | Pro | Thr | Gln | Gly | Ala |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | Pro | Ala | Phe | Ala | Ser | Ala | Phe | Gln | Arg | Arg | Ala | Gly | Gly | Val | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Ala | Ser | His | Leu | Gln | Ser | Phe | Leu | Glu | Val | Ser | Tyr | Arg | Val | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

Arg

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

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CACCTTGCGC AGCCCGACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC
60
TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG
120
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC
180
TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA
240
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG
300
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC
360
TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCCTGC CCTGCAGCCC
420
ACCCAGGGTG CCATGCCGGC CTTGCGCTCT GCTTTCAGC GCCGGGCAGG AGGGGTCCTG
480
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG C
531

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